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(57) Abstract: The present invention provides methods for determining whether a nucleic acid sequence is a marker for a phenotype or cell type of interest which comprises providing a database of expressed sequence tag sequences (EST's) from the species; placing said EST's in groups termed clusters based on homology of EST's within each cluster; determining for each cluster the total number of EST's within said cluster; ordering said clusters sequentially based on the number of EST's in each cluster; dividing said ordered clusters into subranges based on the number of EST's per cluster; determining for each cluster subrange obtained from step (e) the number EST's within said cluster which are expressed in said predetermined cell type of interest; calculating according to a normal distribution the number of clusters in each subrange expected to contain a predetermined threshold percentage of EST's expressed in said cell type of interest, wherein said threshold percentage is a percentage from about 10% to about 100%; determining the number of clusters in each subrange observed to contain said predetermined threshold percentage of EST's expressed in said predetermined cell type; and identifying subranges having an observed number of clusters that meet said predetermined threshold percentage greater than the number of clusters expected to meet said predetermined threshold percentage for the subrange according to normal distribution; wherein if the percentage of EST's expressed in said cell type of interest in a cluster identified is equal to or greater than said predetermined threshold percentage, the cluster contains a nucleic acid that is a marker for the cell type of interest.

IN SILICO SCREENING FOR PHENOTYPE-ASSOCIATED EXPRESSED SEQUENCES

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FIELD OF THE INVENTION

[0001] The present application is related to, and claims the benefit of priority of, Provisional Application No.'s 60/293,999, filed May 30, 2001, 60/330,457, filed October 22, 2001, and 60/357,144, filed February 19, 2002, all of which are incorporated in their entirety by reference
10 herein.

[0002] The invention relates generally to the field of genetics and differential expression of genes of interest. More specifically, the invention relates to methods for detecting expression of nucleic acids or proteins associated with a particular phenotype by performing a differential global comparison of a group of Expressed Sequence Tags (EST's) expressed in a particular tissue or cell
15 type with a larger group of available EST's for a plurality of cell types.

[0003] The publications and other materials used herein to illuminate the background of the invention or provide additional details respecting the practice are incorporated by reference.

BACKGROUND OF THE INVENTION

20 [0004] Comparing patterns of gene expression in different cell lines and tissues has important applications for a variety of biological problems. Such information is useful, for example, in comparing mechanisms of differentiation, microbial pathogenesis or tumor malignancy. Typically, such information is obtained by detecting altered gene or protein expression patterns associated with a particular phenotype. Comparing patterns of expression is particularly important,
25 for example, in determining pattern(s) of expression that lead to aberrant cell growth, especially in tumor formation and cancer. A number of experimental methods have been designed for the detection of phenotype or celltype associated gene expression. Most of them are based on time-consuming and expensive experimental protocols (e.g., numerous modifications of the differential display approach, cDNA microarrays, or Serial Analysis of Gene Expression).

30 [0005] EST's are an integral tool in the study of differential expression patterns. The total number of human ESTs in publicly available databases ($>4 \times 10^6$) exceeds by approximately two orders of magnitude the total number of different transcripts that can be deduced from the number of human genes ($2.5 - 4 \times 10^4$). Accordingly, there presently exists a need for computer-based

procedures for the detection of EST expression profiles to replace traditional experimental protocols utilized in gene expression profiling.

[0006] UniGene is an experimental system for automatically partitioning GenBank sequences into a non-redundant set of gene-oriented EST clusters based on DNA sequence
5 homology. Each UniGene cluster contains homologous or similar sequences that represent a unique "gene" or RNA transcript, as well as related information, such as the tissue type(s) in which expression of the transcript has been detected and the map location of the gene encoding the transcript. In addition to sequences of well-characterized genes, hundreds of thousands of novel EST's are also included in the UniGene partitioning system. Clustering is the process of finding
10 subsets of sequences which belong together within a larger set. This is done by converting discrete similarity scores to boolean links between sequences using techniques well known in the art. That is, two sequences are considered linked if their similarity or homology exceeds a threshold. Sequence pairs which are sufficiently similar are linked together to form initial clusters. The set of ESTs is compared with the set of genes using the "megablast" algorithm (Zhang et al., J Comput
15 Biol;7(1-2):203-14 (2000)) and sufficiently similar sequence pairs are added to a particular cluster. A detailed description of clustering performed in the UniGene system can be found at <http://www.ncbi.nlm.nih.gov/UniGene>.

[0007] Differentially expressed EST clusters may be useful as phenotypic markers and prognostic indicators and may be suitable targets for various therapeutic interventions. Prior art
20 methods for the detection of phenotype or cell type of interest or expression patterns have included pairwise comparison of expression patterns in a the phenotype or cell type of interest and corresponding normal tissue in order to determine transcripts which are expressed either specifically or in higher quantities in the cell type of interest. As an example, such pairwise comparisons have been done for tumor-associated expression patterns.

25 [0008] The technique of computer based differential display (CDD) compares expression patterns in a particular tissue versus another tissue source. The comparison can be based on sequence databases available in the World Wide Web. This technique has been used to identify prostate-associated genes (Vasmatzis et al. Proc.Natl. Acad. Sci. USA 95, 300-304 (1998)) or ectopically expressed genes in particular tumor types in comparison to corresponding normal tissue
30 (Schuerle et al. Cancer Res. 60, 4037-4043 (2000)).

[0009] There presently exists a need to develop computer based methods for comparing

large numbers of EST's in a global fashion with all known phenotype-associated EST's, so that phenotype-associated patterns of gene expression can be culled from the massive number of such sequences available, without the need for an extensive number of microarray analyses or serial analyses of gene expression in a pairwise manner between a cell type of interest and another individual cell type.

SUMMARY OF THE INVENTION

[00010] The present invention provides methods for the detection of nucleic acid markers associated with a cell type or phenotype of interest by performing a global comparison of a group of EST's known to be expressed in the cell type or phenotype of interest with all EST's expressed in normal tissue in order to identify EST's that are preferentially expressed in the cell or phenotype of interest. The methods comprise arranging both the EST's of interest from a particular species and a larger group of other EST's available for the species in clusters based on homology among the EST's. The methods further comprise arranging the clusters into distinct subranges based on the number of EST's in each cluster and, based on the percentage of EST's derived from the cell type of interest, calculating the number of clusters expected to contain a predetermined percentage of EST's from the cell type of interest. Subranges which contain more than the expected number of clusters containing at least or more than the predetermined percentage of EST's from the cell type are selected for further analysis. The present invention also presents a method for determining a computer based differential display (CDD) of cell or phenotype-associated genes. In one embodiment, the cell or phenotype associated markers are determined for a tumor cell. In a preferred embodiment, at least some of the discrete steps in the method are performed on a computer and comparisons are made between global expression patterns of EST's in a specific cell type or phenotype (such as, *e.g.* tumor) versus global expression patterns of EST's in all other tissue. Alternatively, the comparisons can be made between EST's expressed in a specific cell type and EST's expressed in normal tissue. The approach was inspired by the hypothesis that evolutionary selective pressures might provide conditions for expression of genes that are not expressed in normal tissue (Kozlov, Medical Hypotheses 46, 81-84 (1996)).

[00011] In one embodiment, the invention provides methods for the detection of phenotype or cell type-associated markers by global comparison of all phenotype or cell type-associated EST's with all known EST's to identify EST's that are preferentially expressed in cells expressing the

particular phenotype. In a particularly preferred embodiment, the phenotype is tumor formation and the cell type is a tumor cell. Thus, in one embodiment, the invention provides a method for the detection of tumor markers by global comparison of all tumor associated EST's with all known EST's to identify EST's that are preferentially expressed in tumors.

- 5 [00012] In another embodiment, the invention provides a method for the detection of stress-related genes in a plant model relevant to agricultural plants. Thus, in another preferred embodiment, comparisons are made between global expression patterns of EST's in *Arabidopsis thaliana* grown in stress conditions (i.e., drought, cold, high salt concentration) versus global expression patterns of EST's in *A. thaliana* cultivated under normal conditions. Comparisons can
10 also be made between mature plant cells and cells from roots or shoots.
- [00013] Analysis of combined preparations of mRNAs from several tissues in saturation and experimental subtractive hybridization procedures indicate that tumors contain more diverse sets of mRNAs than any normal tissue. This observation led to the idea of subtracting all available normal EST's (instead of pairwise comparisons) from all available tumor and corresponding normal tissue.
15 (Evtushenko et al. Mol.Biol. 23, 510-520 (1989).
- [00014] In one embodiment, the invention provides a method for determining whether a nucleic acid sequence is a marker preferentially expressed in a phenotype or cell type of interest from a biological species. In a preferred embodiment, the invention is performed with the aid of statistical software analysis and one or more computers and comprises the following steps: (a) providing a
20 database of expressed sequence tag sequences (EST's); (b) placing said EST's in groups termed clusters based on homology of EST's within each cluster; (c) determining for each cluster the total number of EST's within said cluster; (d) ordering said clusters sequentially based on the number of EST's in each cluster; (e) dividing said ordered clusters into subranges based on the number of EST's per cluster; (f) determining for each cluster subrange obtained from previous step (e) the
25 number EST's within said cluster which are expressed in said predetermined cell type of interest; (g) calculating according to a normal distribution the number of clusters in each subrange expected to contain a predetermined threshold percentage of EST's expressed in said cell type of interest, wherein said threshold percentage is a percentage from about 10% to about 100%; (h) determining the number of clusters in each subrange observed to contain said predetermined threshold
30 percentage of EST's expressed in said predetermined cell type; and (i) identifying subranges having an observed number of clusters that meet said predetermined threshold percentage greater than the

number of clusters expected to meet said predetermined threshold for the subrange according to normal distribution; wherein if the percentage of EST's expressed in said cell type of interest in a cluster identified in (i) is equal to or greater than said predetermined threshold percentage, said cluster contains a nucleic acid marker preferentially expressed in the cell type of interest. In preferred embodiments, the clusters of the invention are derived from the UniGene database, which contains all sequences associated with a cluster. The clusters have unique "Hs." Unigene cluster ID numbers to identify the cluster based on homology. Thus, once a cluster is identified as associated with a phenotype using the EST's from the cluster, the cluster-identifier can be used to identify all other sequences associated with the cluster such as full length mRNA's that are homologous to the EST's in the cluster. In this manner, a reference nucleic acid or polypeptide sequence for the cluster can be determined by reviewing the Unigen database. The methods of the present invention can be used with any database, as long as the database contains sequences that can be arranged in clusters based on homology.

[00015] In one embodiment, the invention provides a method for determining whether a nucleic acid is a marker in humans preferentially expressed in a tumor cell. In this embodiment, EST's from a database containing human EST's which contain a description of the source of the EST's retrieved from the cluster description are provided and arranged in individual clusters based on homology; for each cluster the total number of EST's within said cluster is determined; said clusters are ordered sequentially based on the number of EST's in each cluster; said ordered clusters are divided into subranges based on the number of EST's per cluster; the number of EST's within said cluster which are expressed in tumors is determined for each cluster subrange; there is then calculated according to a normal distribution the number of clusters in each subrange expected to contain a predetermined threshold percentage of EST's expressed in tumors; wherein said threshold percentage is a percentage from about 90% to about 100%; the number of clusters is determined in each subrange observed to contain said predetermined threshold percentage of EST's expressed in tumors; and subranges having an observed number of clusters that meet said predetermined threshold percentage greater than the number of clusters expected to meet said predetermined threshold for the subrange according to normal distribution are identified; wherein if the percentage of EST's expressed in said cell type of interest in a cluster from a subrange identified as having a greater than expected number of such clusters is equal to or greater than said predetermined threshold percentage, said cluster contains a nucleic acid marker preferentially expressed in tumors.

[00016] In another embodiment, the invention provides a method for detecting EST expression in stress induced *A. thaliana* which comprises the following steps: (a) for all individual *A. thaliana* EST clusters, the number of ESTs is retrieved from the cluster description; (b) next, the number of ESTs from all stress-induced cDNA libraries present in each cluster description is counted; (c) there is then determined for each cluster the total number of EST's within said cluster; (d) said clusters are ordered sequentially based on the number of EST's in each cluster; (e) said ordered clusters are then divided into subranges based on the number of EST's per cluster; (f) it is then determined for each cluster subrange obtained from previous step (e) the number of EST's within said cluster which are expressed in Arabidopsis cells presented with stress conditions; (g) there is then calculated according to a normal distribution the number of clusters in each subrange expected to contain a predetermined threshold percentage of EST's expressed in said cell type of interest, wherein said threshold percentage is a percentage from about 10% to about 100%; (h) the number of clusters in each subrange observed to contain said predetermined threshold percentage of EST's expressed in said predetermined cell type is determined; and (i) subranges having an observed number of clusters that meet said predetermined threshold percentage greater than the number of clusters expected to meet said predetermined threshold for the subrange according to normal distribution are identified; wherein if the percentage of EST's expressed in stress-induced plants in a cluster identified in (i) is equal to or greater than said predetermined threshold percentage, said cluster contains a nucleic acid marker preferentially expressed in the stress-induced plants.

[00017] The invention thus provides a method for correlating EST expression with a phenotype and in one embodiment requires correlation between a central unit or units containing EST sequence information. In a preferred embodiment, at least some of the EST sequence information analysis is implemented on a conventional personal computer, with the correlator being embodied in a software program. Because the correlator is embodied in software, it may be transported among various computers, which may be used separately or together to perform some or all of the various operations discussed herein.

[00018] In another embodiment, the invention provides a method for identifying a tumor cell which comprises detecting the expression of a tumor-associated marker of the present invention. As discussed in greater detail *infra*, the tumor-associated marker can be a nucleic acid or a polypeptide or fragments thereof.

[00019] In another embodiment, the invention provides a method for detecting a tumor cell by detecting the expression of nucleic acid sequences which are tumor-associated and can be used as diagnostic tools for the detection of tumor tissue. The tumor-associated nucleic acids are detected using the methods for determining whether a nucleic acid sequence is a marker for tumors as described herein. The sequences may be utilized for both *in vitro* and *in vivo* screening for the presence of a tumor cell. In one embodiment, the invention provides a method for detecting the expression of a tumor-associated nucleic acid sequence wherein the sequence is selected from the group consisting of SEQ ID NO:'s 9, 11, 13, 15, 17, 19, 23, 25, 27, 29, 33, 35, 37, 39, 41, 45, 47, 55, 57, 59, 61, 63, 65, 67, 69, 73, 75, 77, 79, 81, 83, 89, 91, 93, 95, 97, 99, 101, 103, 107, 109, 111, 113, 115, 117, 119, 121, 123, 127, 129, 131, 133, 135, 137, 138, 140, 142, 144, 146, 148, 150, 153, 155, 157, 158, 160, 162, 164, 166, 168, 172, 174, 176, 178, 180, 182, 184, 186, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, and 414. In a particularly preferred embodiment, the nucleic acid sequence is selected from the group consisting of SEQ ID NO:'s 73, 184, 186 and 242.

[00020] In another embodiment, the invention provides a method for detecting a tumor cell by detecting the expression of an antigen of a tumor-associated polypeptide which comprises screening tissue or cells with antibodies specific for an antigen expressed by a tumor associated polypeptide, wherein the polypeptide is selected from the group consisting of SEQ ID NO:'s 10, 12, 14, 16, 20, 24, 46, 28, 30, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 71, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 124, 126, 128, 130, 132, 134, 136, 139, 141, 143, 145, 147, 149, 151, 152, 154, 156, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 231, 233, 235, 237, 239, 241, 243, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 399, 401, 403, 405,

407, 409, 411, 413 and 415. In a preferred embodiment, the invention provides a method for detecting an antigen expressed by a tumor-associated polypeptide selected from the group consisting of SEQ ID NO:'s 74, 185, 187, 188 and 243.

[00021] In another embodiment, the invention provides a method for regulating the growth of a tumor cell which comprises regulating the expression of a nucleic acid selected from the group consisting of SEQ ID NO:'s 9, 11, 13, 15, 17, 19, 23, 25, 27, 29, 33, 35, 37, 39, 41, 45, 47, 55, 57, 59, 61, 63, 65, 67, 69, 73, 75, 77, 79, 81, 83, 89, 91, 93, 95, 97, 99, 101, 103, 107, 109, 111, 113, 115, 117, 119, 121, 123, 127, 129, 131, 133, 135, 137, 138, 140, 142, 144, 146, 148, 150, 153, 155, 157, 158, 160, 162, 164, 166, 168, 172, 174, 176, 178, 180, 182, 184, 186, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412 and 414. In a particularly preferred embodiment, the nucleic acid sequence is selected from the group consisting of SEQ ID NO:'s 73, 184, 186 and 242.

[00022] In another embodiment, the invention provides a method for regulating the growth of a tumor cell which comprises regulating the expression of a polypeptide selected from the group consisting of SEQ ID NO:'s 10, 12, 14, 16, 20, 24, 46, 28, 30, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 71, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 124, 126, 128, 130, 132, 134, 136, 139, 141, 143, 145, 147, 149, 151, 152, 154, 156, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 231, 233, 235, 237, 239, 241, 243, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 399, 401, 403, 405, 407, 409, 411, 413 and 415. In a preferred embodiment, the invention provides a method for detecting an antigen expressed by a tumor-associated polypeptide selected from the group consisting of SEQ ID NO:'s 74, 184, 185, 187, 188 and 243.

[00023] In another embodiment, the invention provides a method for vaccinating an animal to

protect the animal from developing a tumor which comprises administering to the animal an immunogen comprising a polypeptide encoded by a nucleic acid selected from the group consisting of SEQ ID NO:'s 10, 12, 14, 16, 20, 24, 46, 28, 30, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 71, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 124, 126, 128, 130, 132, 134, 136, 139, 141, 143, 145, 147, 149, 151, 152, 154, 156, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 231, 233, 235, 237, 239, 241, 243, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 399, 401, 403, 405, 407, 409, 411, 413 and 415. In a preferred embodiment, the animal is a human and the immunogen comprises a polypeptide encoded by SEQ ID NO:'s 74, 185, 187, 188 and 243.

DETAILED DESCRIPTION OF THE INVENTION

[00024] In one embodiment, the methods of the present invention can be used to classify data from original dbEST and UNIGENE databases in a table form (Baranova et al., FEBS Letters, 508, 143-148 (2001)). The HSAlyst program is one type of software program that can be used to assemble the EST sequences and clusters using the methods of the present invention. This program is available at (<http://pcn197.vigg.ru/programs/HSAlyst.exe>). In one preferred embodiment, the methods of the invention comprise the compiling of a supplemental database which contains only those sets of EST's that can specifically be associated with expression in either a particular abnormal (e.g., tumor) or normal physiological condition or tissue type. In one embodiment, the supplemental database includes EST entries from all human cDNA libraries that can specifically be classified as «tumor» or «normal» by tissue source. The supplemental database utilized in the demonstrative examples of the present invention contains a carefully checked description of each included library, cross-referenced from different data sources such as dbEST, UNIGENE and CGAP web-sites, which are available at the National Institutes of Health web site (www.ncbi.nlm.nih.gov), TIGR (www.tigr.org) and Stratagene (www.stratagene.com). The supplemental database thus contains a classification of all cDNA libraries as either tumor or normal.

Approximately 4000 entries in the supplemental database describing cDNA sources were classified according to their origin from tumor or normal tissues (cells). In checking the libraries, those obtained from "pre-malignant", "non-cancerous pathology" and "immortalized cells" were not included in the supplemental database. In other embodiments, one or more databases can be utilized in the methods of the invention without modifying in a supplemental database. In the case of the databases used in the demonstrative examples presented herein, some of the libraries were considered undefined due to lack of information or ambiguity of information.

[00025] EST pre-classification in the supplemental databases for other possible tasks not described herein can be performed by users themselves

[00026] HSAlyst software was able to arrange EST data in the supplemental database according to any given parameter, e.g. tissue type or the number of ESTs contained in a cluster. As will readily be appreciated by persons of ordinary skill in the art, classification of ESTs according to tissue types requires verification of available database information on expression patterns and is the most time-consuming stage. Depending on the type of tissue being analyzed for global expression patterns, a specific database may contain and compare only sequences that are conclusively known to be expressed in a given cell type or physiological state. Classification of the data can be performed by many variations of software capable of handling large groups of data from the UniGene database without deviating from the scope of the present invention.

[00027] In one embodiment, the present invention provides a method for the detection of tumor markers wherein the CDD approach is utilized to search various publicly available databases containing human EST's. This gene-hunting procedure was inspired by the hypothesis that tumors may provide conditions for the expression of some transcribed units that are not expressed in any normal tissues. Instead of pairwise comparison of each tumor and corresponding normal tissue, a differential display of all available tumor libraries against all available normal libraries was performed.

[00028] A particular feature of the methods of the present invention includes subtracting all available clusters containing more than 10% of normal-derived ESTS from a whole set of the UniGene clusters to identify clusters associated with a particular phenotype, instead of pairwise comparisons of each tumor and corresponding normal tissue.

[00029] EST's present a particularly useful set of sequence data to analyze with the methods of the present invention. GenBank included 3,900,480 human ESTs as of November 16, 2001.

These sequences and the methods of the present invention were used to generate Table 1 discussed *infra*. UniGene includes all human ESTs clustered by homology. It should be noted that as available sequence data on EST's continues to grow, these numbers correspondingly change. The methods of the present invention will be equally applicable, however, to the evolving database resources which continue to become available for sequence analysis.

[00030] Most EST's can be traced to a certain tissue source, including tumor and normal ones. In a particularly preferred embodiment, the comparison of tumor and normal libraries is performed on a supplemental database referred to herein as "LibraryRegistry", which comprises a supplemental database that contains only those EST's that clearly are defined as originally detected in normal or tumor tissue samples, as discussed above. It can readily be appreciated by persons of ordinary skill in the art that similar methods can be employed to "customize" a database to include only sequences known to be associated with a particular phenotype or cell type and a defined set of "normal" sources which provide sequences that can be distinguished from the cell or phenotype of interest. Just as the present invention provides tumor-associated EST's and compares these to other human EST's, an example is also provided which compares EST's reported from stress-induced Arabidopsis and EST's from Arabidopsis that are not from plants exposed to the stress conditions.

[00031] A preferred embodiment of the invention utilizes a method of sequence comparison to determine tumor-associated EST's. This method is demonstrated on tumor-specific sequences but as noted is applicable to any well-described database which provides information on the origin of nucleic acid sequences contained therein. In the first step, a database of clustered EST sequences containing a description of the source for each of the sequences is selected for analysis. In the second step, for each cluster the number of its ESTs is retrieved from the cluster description. Next, the number of ESTs from the "tumor" cDNA libraries is counted. The whole range of possible EST numbers is dissected into sub ranges. The arrangement of sub ranges can be performed exponentially (e.g., sub ranges with exponents 1-2, 3-4, 5-8, 9-16) or linearly (sub ranges with factors 1-10, 11-20, 21-30). Simultaneously, the tumor ESTs/all ESTs percentage is calculated for each cluster and those clusters which exceed a user-defined bottom threshold value for the percentage of tumor ESTs/all ESTs are listed in the output file as tumor specific clusters.

[00032] The subranges can be arranged exponentially (e.g., sub ranges with exponents 1-2, 3-4, 5-8, 9-16) or linearly (sub ranges e.g. with factors 1-10, 11-20, 21-30). Classification of subranges into linear or logarithmic format provides two complementary ways for statistical

estimation of a threshold level for determining whether a cluster is associated with a particular phenotype. Using the methods of the present invention, arrangement of subranges produced successful detection of tumor-associated markers whether subranges were arranged linearly as in Table 1 or logarithmically. Program output is designed to separate information about each set of clusters of the same size. In general it is possible to choose some intervals within the whole range of cluster sizes (cluster "size" is the number of EST's in a cluster). For example, if one needs the detailed picture of tumor clusters distribution it may be useful to choose narrow intervals, even assigning a cluster to as little as 1 EST sequence. For each interval the following values are calculated: total number of ESTs contained in clusters of the size within the interval N_{EST} , total number of these clusters N_{clust} and the number of tumor related clusters N_{tum} within this interval. Tumor related clusters that have relative content of tumor tissue-derived ESTs over the threshold denoted as «t» given by user (usually from 90% to 100%). Also, the theoretically expected number of tumor clusters within this interval is calculated. To let a computer program do this, the user must input the expected content p of tumor-related ESTs in the whole database. Given the N_{EST} and N_{clust} for the interval it is assumed that tumor cluster distribution is binomial so the expected number of tumor clusters is $N_{tum} = N_{clust} * \sum C_m^n p^m (1-p)^{n-m}$ where p is mean tumor ESTs content in database (declared by user). The sum in the brackets is calculated for each $m: n \geq m \geq t$, where n varies between the interval edges and represents the hypothetical cluster size. The 90-100% threshold range described above for cell type-associated clusters in humans is for the case of human tumor-associated EST's but this number can vary depending on the difference between the expected number of clusters at a given t for a cluster size versus the observed number of clusters at a given t for the cluster size.

[00033] In an exemplary analysis using the methods of the present invention, the database LibraryRegistry was analyzed. This library provided a database of EST's from human normal and tumor sources. The EST's were placed in clusters based on homology; for each cluster the total number of EST's within the cluster was determined, the clusters were then ordered sequentially based on the number of EST's in each cluster and divided into subranges linearly based on the number of EST's per cluster as shown in Table 1. For each cluster subrange obtained the number EST's within said cluster expressed in tumor cells was determined. Next, based on a normal distribution, the number of clusters in each subrange expected to contain a predetermined threshold percentage of EST's expressed in tumor cells was calculated, wherein the threshold percentage was

calculated at 90% and 100%. The number of clusters in each subrange observed to contain 90% or 100% tumor-specific EST's was determined. Next, subranges having an observed number of clusters that meet said predetermined threshold percentage five times greater than the number of clusters expected to meet said predetermined threshold for the subrange according to normal distribution were noted. Clusters in the subranges between 17 and 2048 were determined to contain 5 times or greater the number of expected clusters having 90% or more tumor-derived EST's in the cluster subrange were identified. These clusters were then associated with the corresponding Hs. Identifying number from the Unigene database to determine the nucleic acid sequences which were tumor-associated sequences.

[00034] To be sure that what was found was a "true" tumor-associated cluster not generated by chance among the total number of EST clusters classified with the methods of the present invention, the theoretical number of "tumor" clusters for every sub range is calculated. This is done utilizing an underlying model of a unimodal binomial distribution with the mean value of "tumor/all" percentage that can be defined by the user (0 to 100%). This binomial method is used to determine the expected number of tumor/all for predetermined thresholds for each cluster size based on the proportion of EST's from tumor cells in the database. In the example described in Table 1, the subranges which were analyzed for 90% or more tumor derived EST's were subranges that contained at least five times more such clusters than expected for the cluster size. This ratio of observed to expected has been found by the inventors to be reliable for determining phenotype or cell type associated clusters utilizing databases from Arabidopsis, human and mouse. It will readily be appreciated by persons of ordinary skill in the art that other ratios of observed/expected clusters for a predetermined threshold will also be useful. As little as 3.5 times the number of observed/expected clusters equal to or greater than the threshold range are also contemplated. Clusters between 3.5 and 5 times the number of expected clusters may also identify useful subranges displaying the predetermined threshold percentage of sequences for a cluster. Alternatively, an observed number of clusters for subrange that is at least one standard deviation greater than the number of clusters expected for a subrange may also be used to identify useful subranges displaying the predetermined threshold percentage of sequences for a cluster.

[00035] Referring now to Table I, the expected numbers of tumor-specific clusters that exceeded threshold values were calculated for a UniGene database of human EST's that was available on November 6, 2001. A comparison between the expected and observed tumor-derived

EST's demonstrated that tumor-related clusters were not accidental but represented a natural phenomenon. In this example, user-derived threshold values for the percentage of tumor-derived EST's to all EST's were at least 90% tumor-derived EST's per cluster and 100% tumor-derived EST's per cluster. When at least 90% of the EST's in a cluster are tumor derived, the cluster is referred to as tumor-associated. Each cluster was identified with a representative nucleic acid sequence based on the Hs. number for the sequence and the representative longest nucleotide sequence or defined mRNA sequence associated with the cluster.

[00036] Referring now to Table II, there are shown the results of tumor-related clusters detected with the methods of the present invention on a Unigene database that was assembled May 3, 2002. Except for the methods otherwise noted, the methods used to determine markers for tumors were as described for Table II. All of the tumor associated clusters in Table II had a number of EST's per cluster of 10 or more, which was found to be a significant number of EST's that would be tumor-associated using the methods described herein for identifying subranges having an observed number of clusters that was five times more than the expected number of clusters that met a predetermined threshold of 90% or more tumor derived sequences. Among the 196 tumor related clusters detected, 93 are non-coding and 103 encode at least one polypeptide sequence. Among clusters encoding a polypeptide, six correspond to known genes previously described as tumor markers/antigens, as indicated in Table 2.

[00037] Differentially expressed EST clusters are useful as markers for a physiological state or phenotype and prognostic indicators and may be suitable targets for various therapeutic interventions. Therapeutic interventions can include use of various gene therapy techniques to regulate the expression of the sequences, target-associated antibodies to inhibit growth of cells expressing phenotype associated marker polypeptides, and use of marker polypeptides as immunogens to vaccinate an animal against cells expressing the marker.

[00038] Useful diagnostic techniques include, but are not limited to fluorescent in situ hybridization (FISH), direct DNA sequencing, PFGE analysis, Southern blot analysis, single stranded conformation analysis (SSCA), RNase protection assay, allele-specific oligonucleotide (ASO), dot blot analysis and PCR-SSCP, as discussed in detail further below. Also useful is the recently developed technique of DNA microchip technology.

[00039] "Antibodies." The present invention also provides polyclonal and/or monoclonal antibodies and fragments thereof, and immunologic binding equivalents thereof, which are capable

of specifically binding to the tumor-associated polypeptides and fragments thereof or to polynucleotide sequences from the tumor-associated region, particularly from the tumor-associated locus or a portion thereof. The term "antibody" is used both to refer to a homogeneous molecular entity, or a mixture such as a serum product made up of a plurality of different molecular entities.

5 Antibodies to the tumor-associated markers will be useful in assays as well as pharmaceuticals.

[00040] As used herein, the term "computer" is meant to refer to at least one computer but can also include more than one computer connected by any means known in the art of computer science. Furthermore, the term is also meant to include a computer interacting with a remote computer or other server which provides access to a plurality of databases via the world wide web.

10 In one embodiment, the analysis of EST clusters is performed on software on a computer, while the information imported to the computer for correlation is obtained from contact with the world wide web.

[00041] Alteration of mRNA expression for the tumor markers of the present invention can be detected by any techniques known in the art. These include Northern blot analysis, PCR amplification and RNase protection. Alteration of expression of tumor-associated genes can also be detected by screening for alteration of the expression of the protein encoded by a tumor-associated gene. For example, monoclonal antibodies immunoreactive with a marker polypeptide can be used to screen a tissue using methods known in the art. These include Western blots, immunohistochemical assays and ELISA assays. Functional assays, such as protein binding determinations, can be used and assays biochemical function of a tumor-associated marker can be employed.

[00042] Genes or gene products can also be detected in human body samples, such as serum, stool, urine and sputum and isolated tumor tissue. The same techniques discussed above for detection of genes or gene products in tissues can be applied to other body samples. Cancer cells are sloughed off from tumors and appear in such body samples. In addition, the gene product itself may be secreted into the extracellular space and found in these body samples even in the absence of cancer cells. By screening such body samples, a simple early diagnosis can be achieved for many types of cancers. In addition, the progress of chemotherapy or radiotherapy can be monitored more easily by testing such body samples for genes or gene products. The diagnostic methods of the present invention is useful for clinicians, so they can decide upon an appropriate course of treatment.

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[00043] Pairs of single-stranded DNA primers can be annealed to sequences within or surrounding a tumor-associated gene in order to prime amplifying DNA synthesis of the gene itself. A complete set of these primers allows synthesis of all of the nucleotides of the gene coding sequences, i.e., the exons. The set of primers preferably allows synthesis of both intron and exon sequences. The primers themselves can be synthesized using techniques which are well known in the art. Generally, the primers can be made using oligonucleotide synthesizing machines which are commercially available. Given the sequences of the tumor associated genes of the invention, design of particular primers is well within the skill of the art.

[00044] The nucleic acid probes provided by the present invention are useful for a number of purposes. They can be used as probes to detect PCR amplification products derived from the mRNA of the gene or to detect actual mRNA transcripts directly in tumors or other cells being analyzed for expression of tumor-associated markers.

[00045] "Probes". Polynucleotide probes form a stable hybrid with a of the target sequence, under highly stringent to moderately stringent hybridization and wash conditions. If it is expected that the probes will be perfectly complementary to the target sequence, high stringency conditions will be used. Hybridization stringency may be lessened if some mismatching is expected, for example, if variants are expected with the result that the probe will not be completely complementary. Conditions are chosen which rule out nonspecific/adventitious bindings, that is, which minimize noise. In general, hybridizations conditions will be stringent conditions.

[00046] Probes for the tumor-associated markers may be derived from the sequences of the region or its cDNAs. The probes may be of any suitable length, which span all or a portion of the marker, and which allow specific hybridization to the transcripts expressed from the marker. If the target sequence contains a sequence identical to that of the probe, the probes may be short, e.g., in the range of about 8-30 base pairs, since the hybrid will be relatively stable under even highly stringent conditions. If some degree of mismatch is expected with the probe, i.e., if it is suspected that the probe will hybridize to a variant region, a longer probe may be employed which hybridizes to the target sequence with the requisite specificity.

[00047] The probes may include an isolated polynucleotide attached to a label or reporter molecule and may be used to isolate other polynucleotide sequences, having sequence similarity by standard methods. Other similar polynucleotides may be selected by using homologous polynucleotides. Alternatively, polynucleotides encoding these or similar polypeptides may be

synthesized or selected by use of the redundancy in the genetic code. Various codon substitutions may be introduced, e.g., by silent changes (thereby producing various restriction sites) or to optimize expression for a particular system.

[00048] Probes comprising synthetic oligonucleotides or other polynucleotides of the present invention may be derived from naturally occurring or recombinant single- or double-stranded polynucleotides, or be chemically synthesized. Probes may also be labeled by nick translation, Klenow fill-in reaction, or other methods known in the art.

[00049] Portions of the polynucleotide sequence having at least about eight nucleotides, usually at least about 15 nucleotides, and fewer than about 6 kb, usually fewer than about 1.0 kb, from a polynucleotide sequence encoding the tumor associated markers of the invention are preferred as probes. Thus, this definition includes probes of 8, 12, 15, 20, 25, 40, 60, 80, 100, 200, 300, 400 or 500 nucleotides or probes having any number of nucleotides within these ranges of values (e.g., 9, 10, 11, 16, 23, 30, 38, 50, 72, 121, etc., nucleotides), or probes having more than 500 nucleotides. The probes may also be used to determine whether mRNA encoding a tumor-associated marker is present in a cell or tissue. The present invention contemplates the use of probes having at least 8 nucleotides derived from a tumor-associated marker of the invention and any combination of these sequences as described in further detail below, its complement or functionally equivalent nucleic acid sequences.

[00050] Similar considerations and nucleotide lengths are also applicable to primers which may be used for the amplification of all or part of the tumor-associated markers of the invention. Thus, a definition for primers includes primers of 8, 12, 15, 20, 25, 40, 60, 80, 100, 200, 300, 400, 500 nucleotides, or primers having any number of nucleotides within these ranges of values (e.g., 9, 10, 11, 16, 23, 30, 38, 50, 72, 121, etc. nucleotides), or primers having more than 500 nucleotides, or any number of nucleotides between 500 and 9000. The primers may also be used to determine whether mRNA encoding a tumor-associated marker is present in a cell or tissue.

[00051] Nucleic acid hybridization will be affected by such conditions as salt concentration, temperature, or organic solvents, in addition to the base composition, length of the complementary strands, and the number of nucleotide base mismatches between the hybridizing nucleic acids, as will be readily appreciated by those skilled in the art. Stringent temperature conditions will generally include temperatures in excess of 30°C, typically in excess of 37°C, and preferably in

excess of 45°C. Stringent salt conditions will ordinarily be less than 1000 mM, typically less than 500 mM, and preferably less than 200 mM. However, the combination of parameters is much more important than the measure of any single parameter.

[00052] Probe sequences may also hybridize specifically to duplex DNA under certain

5 conditions to form triplex or other higher order DNA complexes. The preparation of such probes and suitable hybridization conditions are well known in the art.

Methods of Use: Nucleic Acid Diagnosis and Diagnostic Kits

[00053] In order to detect the presence of neoplasia, the progression toward malignancy of a precursor lesion, or as a prognostic indicator, a biological sample of the lesion is prepared and
10 analyzed for the presence or absence of the expression of a tumor-associated marker. Results of these tests and interpretive information are returned to the health care provider for communication to the tested individual. Such diagnoses may be performed by diagnostic laboratories, or, alternatively, diagnostic kits are manufactured and sold to health care providers or to private individuals for self-diagnosis.

15 [00054] Initially, the screening method may involve amplification of the relevant sequences. In another preferred embodiment of the invention, the screening method involves a non-PCR based strategy. Both PCR and non-PCR based screening strategies can detect target sequences with a high level of sensitivity.

[00055] The most popular method used today is target amplification. Here, the target nucleic
20 acid sequence is amplified with polymerases. One particularly preferred method using polymerase-driven amplification is the polymerase chain reaction (PCR). The polymerase chain reaction and other polymerase-driven amplification assays can achieve over a million-fold increase in copy number through the use of polymerase-driven amplification cycles. Once amplified, the resulting nucleic acid can be sequenced or used as a substrate for DNA probes.

25 [00056] When the probes are used to detect the presence of the target sequences, the biological sample to be analyzed, such as blood or serum, may be treated, if desired, to extract the nucleic acids. The sample nucleic acid may be prepared in various ways to facilitate detection of the target sequence; e.g. denaturation, restriction digestion, electrophoresis or dot blotting. The targeted region of the analyte nucleic acid usually must be at least partially single-stranded to form
30 hybrids with the targeting sequence of the probe. If the sequence is naturally single-stranded, denaturation will not be required. However, if the sequence is double-stranded, the sequence will

probably need to be denatured. Denaturation can be carried out by various techniques known in the art.

[00057] Analyte nucleic acid and probe are incubated under conditions which promote stable hybrid formation of the target sequence in the probe with the putative targeted sequence in the analyte. The region of the probes which is used to bind to the analyte can be made completely complementary to a targeted region. Therefore, high stringency conditions are desirable in order to prevent false positives. However, conditions of high stringency are used only if the probes are complementary to regions of the chromosome which are unique in the genome. The stringency of hybridization is determined by a number of factors during hybridization and during the washing procedure, including temperature, ionic strength, base composition, probe length, and concentration of formamide. Under certain circumstances, the formation of higher order hybrids, such as triplexes, quadraplexes, etc., may be desired to provide the means of binding target sequences.

[00058] Detection, if any, of the resulting hybrid is usually accomplished by the use of labeled probes. Alternatively, the probe may be unlabeled, but may be detectable by specific binding with a ligand which is labeled, either directly or indirectly. Suitable labels, and methods for labeling probes and ligands are known in the art, and include, for example, radioactive labels which may be incorporated by known methods (e.g., nick translation, random priming or kinasing), biotin, fluorescent groups, chemiluminescent groups (e.g., dioxetanes, particularly triggered dioxetanes), enzymes, antibodies and the like. Variations of this basic scheme are known in the art, and include those variations that facilitate separation of the hybrids to be detected from extraneous materials and/or that amplify the signal from the labeled moiety. A number of these variations are reviewed in e.g., U.S. Patent 4,868,105, and in EPO Publication No. 225,807.

[00059] Once a sufficient quantity of desired tumor-associated polypeptide has been obtained, it may be used for various purposes. A typical use is the production of antibodies specific for binding. These antibodies may be either polyclonal or monoclonal, and may be produced by in vitro or in vivo techniques well known in the art. For production of polyclonal antibodies, an appropriate target immune system, typically mouse or rabbit, is selected. Substantially purified antigen is presented to the immune system in a fashion determined by methods appropriate for the animal and by other parameters well known to immunologists. Typical sites for injection are in footpads, intramuscularly, intraperitoneally, or intradermally. Of course, other species may be substituted for mouse or rabbit. Polyclonal antibodies are then purified using techniques known in

the art, adjusted for the desired specificity.

[00060] An immunological response is usually assayed with an immunoassay. Normally, such immunoassays involve some purification of a source of antigen, for example, that produced by the same cells and in the same fashion as the antigen. A variety of immunoassay methods are well known in the art.

[00061] Monoclonal antibodies with affinities of 10^{-8} M-1 or preferably 10^{-9} to 10^{-10} M-1 or stronger will typically be made by standard procedures. Briefly, appropriate animals will be selected and the desired immunization protocol followed. After the appropriate period of time, the spleens of such animals are excised and individual spleen cells fused, typically, to immortalized myeloma cells under appropriate selection conditions. Thereafter, the cells are clonally separated and the supernatants of each clone tested for their production of an appropriate antibody specific for the desired region of the antigen.

[00062] Other suitable techniques involve in vitro exposure of lymphocytes to the antigenic polypeptides, or alternatively, to selection of libraries of antibodies in phage or similar vectors. The polypeptides and antibodies of the present invention may be used with or without modification. Frequently, polypeptides and antibodies will be labeled by joining, either covalently or non-covalently, a substance which provides for a detectable signal. A wide variety of labels and conjugation techniques are known and are reported extensively in both the scientific and patent literature. Suitable labels include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent agents, chemiluminescent agents, magnetic particles and the like. Patents teaching the use of such labels include U.S. Patents 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149 and 4,366,241. Also, recombinant immunoglobulins may be produced (see U.S. Patent 4,816,567).

Methods of Use: Peptide Diagnosis and Diagnostic Kits

[00063] Antibodies (polyclonal or monoclonal) may be used to detect the absence or presence of peptides encoded by tumor-associated markers of the invention. Techniques for raising and purifying antibodies are well known in the art and any such techniques may be chosen to achieve the preparations claimed in this invention. In a preferred embodiment of the invention, antibodies will immunoprecipitate proteins from solution as well as react with proteins on Western or immunoblots of polyacrylamide gels. In another preferred embodiment, antibodies will detect tumor-associated proteins in paraffin or frozen tissue sections, using immunocytochemical

techniques. Antibodies specific to tumor-associated markers described herein can be employed in conjunction with toxic products that can be bound to the antibodies and selectively delivered to tumor cells via binding of the antibody with the tumor-associated polypeptide present on or in the tumor cell utilizing techniques well known in the art.

5 [00064] Preferred embodiments relating to methods for detecting tumor-associated proteins include enzyme linked immunosorbent assays (ELISA), radioimmunoassays (RIA), immunoradiometric assays (IRMA) and immunoenzymatic assays (IEMA), including sandwich assays using monoclonal and/or polyclonal antibodies. Exemplary sandwich assays are described by David et al. in U.S. Patent Nos. 4,376,110 and 4,486,530.

10 Methods of Use: Antisense and siRNA Therapy

[00065] The present invention contemplates an antisense polynucleotide up to about 50 nucleotides in length that hybridizes with mRNA molecules that encode a tumor-associated polypeptide, and the use of one or more of those polynucleotides in treating cancer cells. See U.S. Patent Nos. 5,891,858 and 5,885,970, incorporated herein by reference, for further details. The
15 antisense polynucleotide or siRNA is useful for treating cancer caused by expression of a tumor-specific or tumor-associated polypeptide. In a similar manner, siRNA molecules specific for tumor-associated nucleic acid markers of the invention can also be used to suppress transcription of said marker sequences.

[00066] In one embodiment an antisense polynucleotide or siRNA is contacted with a cancer
20 cell. The contact is carried out in vivo in a host animal, and contact is effected by administration to the animal of a pharmaceutical composition containing the polynucleotide dissolved or dispersed in a physiologically tolerable diluent so that a body fluid such as blood or lymph provides at least a portion of the aqueous medium. In vivo contact is maintained until the polynucleotide is eliminated from the mammal's body by a normal bodily function such as excretion in the urine or feces or
25 enzymatic breakdown. The polynucleotide may be injected directly into the tumor in an aqueous medium (an aqueous composition) via a needle or other injecting means and the composition is injected throughout the tumor as compared to being injected in a bolus. For example, an aqueous composition containing an antisense polynucleotide or siRNA, the inverts or mixtures thereof is injected into tumors via a needle. The needle is placed in the tumors and withdrawn while
30 expressing the aqueous composition within the tumor. That mode of administration is carried out in three approximately orthogonal planes in the tumors.

[00067] This administration technique has the advantages of delivering the polynucleotide directly to the site of action and avoids most of the usual body mechanisms for clearing drugs. Tumors can be located using *e.g.*, modern imaging techniques such as X-ray, ultrasound and MRI so that exact placement of the polynucleotide can be carried out.

5 [00068] A polynucleotide can also be administered in the form of liposomes. As is shown in the art, liposomes are generally derived from phospholipids or other lipid substances. Liposomes are formed by mono or multi-lamellar hydrated liquid crystals that are dispersed in an aqueous medium. Any non-toxic, physiologically acceptable and metabolizable lipid capable of forming liposomes can be used. The present compositions in liposome form can contain stabilizers, preservatives,
10 excipients, and the like in addition to the agent.

[00069] An antisense polynucleotide or siRNA can also be administered by gene therapy. The polynucleotide may be introduced into the cell in a vector such that the polynucleotide remains extrachromosomal. In such a situation, the polynucleotide will be expressed by the cell from the extrachromosomal location. Vectors for introduction of polynucleotides for extrachromosomal
15 maintenance are known in the art, and any suitable vector may be used. Methods for introducing DNA into cells such as electroporation, calcium phosphate coprecipitation and viral transduction are known in the art, and the choice of method is within the competence of a person of ordinary skill in the art.

[00070] The antisense polynucleotide or siRNA, may be employed in gene therapy methods
20 in order to decrease the amount of the expression products in cancer cells, especially in those cases where overexpressed. Such gene therapy is particularly appropriate for use in both cancerous and pre-cancerous cells.

[00071] Gene therapy would be carried out according to generally accepted methods, for example, as described in further detail in U.S. Patent No. 5,747,282 and references cited therein, all
25 incorporated by reference herein. Expression vectors in the context of gene therapy are meant to include those constructs containing sequences sufficient to express a polynucleotide that has been cloned therein. In viral expression vectors, the construct contains viral sequences sufficient to support packaging of the construct. If the polynucleotide encodes an antisense polynucleotide or siRNA or a ribozyme, expression will produce the antisense polynucleotide or siRNA or ribozyme.
30 Thus in this context, expression does not require that a protein product be synthesized. In addition to the polynucleotide cloned into the expression vector, the vector also contains a promoter

functional in eukaryotic cells. The cloned polynucleotide sequence is under control of this promoter. Suitable eukaryotic promoters include those described above. The expression vector may also include sequences, such as selectable markers and other sequences conventionally used.

[00072] Gene transfer techniques which target DNA directly to specific tumor cell types are preferred. Receptor-mediated gene transfer, for example, is accomplished by the conjugation of DNA (usually in the form of covalently closed supercoiled plasmid) to a protein ligand via polylysine. Ligands are chosen on the basis of the presence of the corresponding ligand receptors on the cell surface of the target cell/tissue type. These ligand-DNA conjugates can be injected directly into the blood if desired and are directed to the target tissue where receptor binding and internalization of the DNA-protein complex occurs. To overcome the problem of intracellular destruction of DNA, coinfection with adenovirus can be included to disrupt endosome function.

Methods of Use: Transformed Hosts; Transgenic/Knockout Animals and Models

[00073] In one embodiment of the invention, a transgene is introduced into a non-human host to produce a transgenic animal expressing a human or murine tumor-specific or tumor-associated gene. The transgenic animal is produced by the integration of the transgene into the genome in a manner that permits the expression of the transgene. Methods for producing transgenic animals are generally described e.g., in U.S. Patent No. 4,873,191.

[00074] Transgenic animals may be produced from the fertilized eggs from a number of animals including, but not limited to reptiles, amphibians, birds, mammals, and fish. Within a particularly preferred embodiment, transgenic mice are generated which overexpress the polypeptide. Alternatively, the absence of the polypeptide in «knock-out» mice permits the study of the effects that loss of protein has on a cell in vivo. Knock-out mice also provide a model for the development of cancers.

[00075] Methods for producing knockout animals have been described previously. The production of conditional knockout animals, in which the gene is active until knocked out at the desired time is also known by those of ordinary skill in the art.

[00076] As noted above, transgenic animals and cell lines derived from such animals may find use in certain testing experiments. In this regard, transgenic animals and cell lines capable of expressing a tumor-specific or tumor-associated gene may be exposed to test substances. These test substances can be screened for the ability to reduce overexpression of the gene or impair the expression or function of a protein encoded by the gene.

[00077] In another embodiment, the invention provides a method for assaying expression of EST's utilizing microarrays comprising antibodies to the tumor-associated EST's of the invention.

[00078] In another embodiment, the invention provides a method for assaying for tumor EST's utilizing microarrays containing polypeptides or fragments thereof encoded and expressed by the tumor-associated EST's of the invention.

[00079] In another embodiment, the invention provides a method for assaying for tumor-associated EST's utilizing microarrays comprising nucleic acids specific for the tumor-related EST's of the invention.

[00080] The newly developed technique of nucleic acid analysis via microchip technology is also applicable to the present invention. In this technique, literally thousands of distinct oligonucleotide probes are built up in an array on a silicon chip. Nucleic acid to be analyzed is fluorescently labeled and hybridized to the probes on the chip. It is also possible to study nucleic acid-protein interactions using these nucleic acid microchips. Using this technique one can determine the presence of a sequence or expression levels of a gene of interest. The method is one of parallel processing of many, even thousands, of probes at once and can tremendously increase the rate of analysis.

[00081] It is also known in to persons of ordinary skill in the art that microchip technology is applicable to screening large numbers of samples by detecting antibody/antigen interactions. Utilizing cell type specific transcripts detected with the methods of the present invention, large numbers of cells from different stages of expression can be screened for expression of antigens. For a general description, see e.g., U.S. patent No. 6,379,895.

[00082] The nucleic acid, protein or antibody to the protein encoded by the nucleic acid may also be incorporated on a microarray. The preparation and use of microarrays are well known in the art. Generally, the microarray may contain the entire nucleic acid or protein, or it may contain one or more fragments of the nucleic acid or protein. Similarly, the microarray may contain an antibody or only the portion of the antibody necessary for binding antigen. It is contemplated by the invention that single chain antibodies may be utilized in the detection of tumor antigen or portions thereof. Suitable nucleic acid fragments may include at least 17 nucleotides, at least 21 nucleotides, at least 30 nucleotides or at least 50 nucleotides of the nucleic acid sequence, particularly where the nucleic acid marker comprises a coding sequence. Suitable protein fragments may include at least 4

amino acids, at least 8 amino acids, at least 12 amino acids, at least 15 amino acids, at least 17 amino acids or at least 20 amino acids.

[00083] In another embodiment, the invention provides methods for vaccinating an animal with tumor-associated polypeptides of the invention as an immunogen. A method of vaccination can comprise administering at least a fragment of a polypeptide encoded by the tumor-associated markers of the present invention. Methods for the administration of such fragments of a peptide are known to a person of ordinary skill in the art and can include administering additional peptide sequences as an adjuvant. In a preferred embodiment, the peptides are administered under conditions which will elicit a cytotoxic T-cell response to a tumor expressing a tumor-associated marker described in the present invention.

[00084] Cytotoxic T Lymphocytes (CTL) are an important means by which a mammalian organism defends itself against cancer. Functional studies of viral and tumor-associated T cells have confirmed that a minimal cytotoxic epitope consisting of a peptide of 8-12 amino acids can prime an antigen presenting cell to be lysed by CD8⁺ CTL, as long as the antigen presenting cell presents the epitope in the context of the correct MHC molecule. It is contemplated that the immunogen may comprise a minimal cytotoxic epitope on the tumor marker polypeptide. Minimal cytotoxic epitopes generally have been most effective when administered in the form of a lipidated peptide together with a helper CD4 epitope. Peptides administered alone, however, also can be highly effective.

[00085] As used herein, the singular form "a", "an", "said" and "the" include plural references unless the context clearly indicates otherwise. For example, a reference to a "cell" would include a plurality of cells.

[00086] As used herein, the terms "diagnosing" or "prognosing," as used in the context of neoplasia, are used to indicate 1) the classification of lesions as neoplasia, 2) the determination of the severity of the neoplasia, or 3) the monitoring of the disease progression, prior to, during and after treatment.

[00087] "Encode". A polynucleotide is said to "encode" a polypeptide if, in its native state or when manipulated by methods well known to those skilled in the art, it can be transcribed and/or translated to produce the mRNA for and/or the polypeptide or a fragment thereof. The anti-sense strand is the complement of such a nucleic acid, and the encoding sequence can be deduced therefrom.

[00088] "Isolated" or "substantially pure". An "isolated" or "substantially pure" nucleic acid (e.g., an RNA, DNA or a mixed polymer) is one which is substantially separated from other cellular components which naturally accompany a native human sequence or protein, e.g., ribosomes, polymerases, many other human genome sequences and proteins. The term embraces a nucleic acid sequence or protein which has been removed from its naturally occurring environment, and includes recombinant or cloned DNA isolates and chemically synthesized analogs or analogs biologically synthesized by heterologous systems.

[00089] As used herein, the terms "tumor-associated marker" and "stress-associated marker" are meant to include nucleic acids or fragments thereof and polypeptides or fragments thereof that are specifically disclosed herein as associated with the indicated phenotype, as well as other nucleic acids or polypeptides or fragments thereof that comprise said polypeptides and nucleic acids and fragments thereof that can be detected with the methods of the present invention and are not known in the prior art to be associated with the particular phenotype.

[00090] As used herein, phenotype associated "marker expression" is meant to include the expression of all or a fragment of a specific (e.g., tumor-specific) or associated (e.g., tumor-associated) marker. Thus, as will be recognized by those of ordinary skill in the art, detection of marker expression is meant to include all known methods for detecting of gene expression, including but not limited to e.g., detecting the expression of an mRNA or fragment thereof (e.g., an EST) for the marker or detecting the expression of a polypeptide or fragment thereof encoded by a tumor associated marker of the invention. Polypeptide or fragments thereof can be detected by antibodies which specifically bind to the polypeptide or fragment thereof and allow its detection in various assay as known in the art such as Western blots, ELISA and the like.

[00091] The practice of the present invention employs, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, genetics, immunology, cell biology, cell culture and transgenic biology, which are within the skill of the art.

General Methods

[00092] **MTC panels.** We used CLONTECH Multiple Tissue cDNA (MTC™) panels, which contain sets of normalized first-strand cDNA generated using CLONTECH Premium RNA™ from different human tumors and normal tissues. These tissue-specific first strand cDNA's were used as

templates in conjunction with tissue-specific tumor EST-derived primers in PCR studies to determine if tumor-associated EST's detected with the methods of the present invention were. The following panels were used: Human Tumor MTC Panel (K1422-1), Human MTC Panel I (K1420-1), Human MTC Panel II (K1421-1), Human Immune System MTC Panel (K1426-1), and Human Fetal MTC Panel (K1425-1).

[00093] **PCR analysis.** PCR of genomic DNA was carried out in 25 μ l of the following reaction mixture: 67mM Tris-HCl (pH 8.9), 4mM MgCl₂, 16mM (NH₄)SO₄, 10mM 2-mercaptoethanol, 0.1 mg/ml BSA, 200 μ M (each) dNTP, specific forward and reverse primers (10 pmol each), 2.5U Taq polymerase, and 500 ng of genomic DNA. The samples were incubated in a PTC-200 thermocycler (MJ Research, USA) for the total of 35 cycles. Each cycle consisted of 30 s at 95°C, 30 s at 56°C for forw/rev16 or at 58°C for forw/rev8, forw/rev19, and forw/rev28, and 1 min at 72°C. DNA primers for PCR sequencing and the size of fragments generated for each cluster sequence were as follows:

Hs.154173:

forward16: (SEQ ID NO:1) 5'-TCT TTC TTG ATG AAT TAT CTT ATG-3'; reverse16: (SEQ ID NO:2) 5'-ACA CAC CCT CAT TCC CGC-3'; fragment size: 443 bp.

Hs. 133294:

forward8: (SEQ ID NO:3) 5'-GTC AAC CTT CTC ATC TTC CTC-3'; reverse8: (SEQ ID NO:4) 5'-CAG GAA GTT GGG TAGATG TG-3'; fragment size: 1) 412 bp fragment size: 2) 1084 bp.

Hs. 67624:

forward19: (SEQ ID NO:5) 5'-TAA TTG CAT TCT TCA AAA TTC TAC-3'; reverse19: (SEQ ID NO:6) 5'-GCT TCG CAC CAT TGAATA AAC-3'; fragment size: 315 bp.

Hs.133107:

forward 28: (SEQ ID NO:7) 5'-TAC ATA GTT GTT ATC TTA AGG TG-3';

reverse 28: (SEQ ID NO:8) 5'-TGG GAA TTC TAT ACT TTT GAC-3'; fragment size: 344 bp.

[00094] The expression of nucleotide sequences under study was analyzed in different tissues using CLONTECH cDNA panels and Titanium Taq PCR kit (K1915-I). Reaction mixtures of a 25- μ l volume were prepared according to the manufacturer's instructions for cDNA panels. PCR was carried out under the following conditions: 1 min at 95°C, 35 cycles consisting of 30 s at 95°C, 30 s at 56°C, for forw/rev16 or at 58°C, for forw/rev8, forw/rev19, or forw/rev28, and. 1 min at 68°C. The terminal stage of the reaction was 5 min at 68°C.

[00095] **Electrophoresis.** The amplification products were separated by electrophoresis in 2% agarose gel and detected by staining with ethidium bromide. 8 μ l of PCR mixture was taken per lane.

[00096] **Computer programs.** Homology searches were performed using BLAST computer
5 programs on a NCBI server (www.ncbi.nlm.nih.gov). Exon-intron boundaries and putative gene elements were predicted using program tools using techniques well known in the art and described in detail for example at the WebGene server (<http://www.itba.mi.cnr.it/webgene/>) and on the search engine of Baylor College of Medicine. (<http://kiwi.imgen.bcm.tmc.edu:8088/search-launcher/launcher.html>).

10 Determination of exon-intron boundaries are indicative of genes as transcribed genomic units producing pre-mRNA spliced during RNA maturation.

[00097] The present invention is described by reference to the following Examples, which are offered by way of illustration and are not intended to limit the invention in any manner. Standard techniques well known by persons of ordinary skill in the art and/or the techniques specifically
15 described herein were utilized.

EXAMPLE 1

[00098] Utilizing publicly available EST sequence data and HSAlyst, available clusters were organized into the ranges shown in Table 1. The software utilized in this example made
20 possible the arrangement of sub ranges exponentially (e.g., sub ranges with exponents 1-2, 3-4, 5-8, 9-16) or linearly (sub ranges with factors 1-10, 11-20, 21-30). In this Example, the sub ranges were arranged linearly. Totally, 2681 libraries were classified as "tumor" libraries, while 1087 libraries were classified as "normal". The supplemental database resulting from this differential comparison contained 921,237 "tumor" ESTs and 810,097 "normal" ESTs. Of these, 83 EST clusters were
25 identified as putative tumor markers, possessing a percentage of tumor-specific EST's/total EST's of at least 90%. The classes of tumor related EST clusters revealed by the methods of the present invention were further classified into five distinct categories based on information provided about the sequences in the public databases, as detailed below in Tables 3-6. The clusters found to be tumor related included non-coding mRNAs, non-coding mRNAs with strict tumor specific
30 expression, genes that encode proteins with weak homology to known proteins (as used herein, "weak refers to statistically significant homology that is not indicative of function or inclusion in

the same gene family), genes that encode known proteins and genes that encode known proteins with a tumor associated expression. In some instances, EST clusters are tumor specific, not being expressed in the normal EST libraries. In other instances, the tumor EST's detected are tumor related, i.e., expressed at significantly higher levels in tumor cells versus normal cell sources. Table 1 represents an analysis of the number of tumor-associated EST's observed with the methods of the present invention.

Table I

Sub-range of # of EST's per cluster	BST number		Tumor specific EST's, %	Number of tumor-specific clusters at threshold, %*			
	# EST's per sub-range	# clusters per sub-range		>90%		100%	
				Observed	Expected	Observed	Expected
1-2	59111	44373	42%	18342	23073	18342	23073
3-4	45400	13401	35%	1880	1884	1880	1884
5-8	53569	8742	37%	567	279	567	172
9-16	63421	5407	39%	168	5	99	4
17-32	83968	3607	41%	45	0	17	0
33-64	176845	3762	43%	16	0	2	0
65-128	349008	3790	45%	10	0	2	0
129-256	460493	2588	47%	8	0	0	0
257-512	339482	975	50%	3	0	0	0
513-1024	208171	303	53%	1	0	0	0
1025-2048	130524	96	57%	0	0	0	0
2049-4096	95180	36	60%	0	0	0	0
4097-8192	49804	10	66%	0	0	0	0
8193-16384	14725	1	67%	0	0	0	0

[00099] An exemplary method for detecting tumor-associated EST's comprised retrieving sequence data on EST's from all available EST's, arranging the EST's into individual clusters based on homology, identifying EST's expressed in tumor cells and, for each cluster, calculating the percentage of the number of ESTs expressed in tumor cells to all EST's contained in the cluster. A threshold value for the percentage of the number of ESTs expressed in tumor cells to all ESTs for each cluster was chosen to identify tumor related clusters. In one example, the percentage of tumor-derived EST's to normal EST's per cluster was a user-defined threshold of at least 90%. Clusters having a percentage of EST's expressed in tumor cells to all EST's for a cluster greater than the threshold value were considered as tumor-associated. Thus, tumor-associated markers represent those nucleic acid or polypeptide or fragments thereof that comprise at least 90% of the sequences in an EST cluster. Some sequences observed were markers that represented nucleic acid or polypeptides or fragments thereof that comprised 100 % of the sequences in a cluster.

[000100] In Table I, there are shown the results of detection of clusters observed at different ranges, with the number of observed tumor related clusters observed versus the number calculated or expected. Clusters were sorted into ranges on a linear basis in this example.

[000101] Using global analysis of cluster data with the methods of the present invention, it has been demonstrated that the sequences of Table 2 represent tumor-associated sequences.

TABLE II

UNIGENE ID	GENE NAME	TUMOR TYPES	SURFACE, IF KNOWN KNOWN TUMOR MARKER INDICATED	REFERENCE NUCLEOTIDE SEQUENCE	REFERENCE PROTEIN SEQUENCE(S)
Hs.203	CCER (Cholecystokinin B receptor)	Choriocarcinoma, glioma, germ cell tumors, lung carcinoma, teratocarcinoma	SURFACE	SEQ. ID NO: 9	SEQ. ID NO: 10
Hs.419	DLX2(Distal-less homeo box 2)	small cell lung carcinoma, pancreatic carcinoma, intestinal carcinoma, ovary carcinoma		SEQ. ID NO: 11	SEQ. ID NO: 12
Hs.560	APOBEC1 ApolipoproteinB mRNA editing enzyme, catabolic polypeptide 1	colon carcinoma; B-cell chronic lymphocytic leukemia;		SEQ. ID NO: 13	SEQ. ID NO: 14
Hs.575	ALDH3A1 (Aldehydehydrogenase 3 family, member A1)	Pancreatic carcinoma, glioma, cervical carcinoma, lung carcinoma, uterine carcinoma, germ cell tumors, gastric carcinoma, colon carcinoma, salivary gland carcinoma, bladder carcinoma		SEQ. ID NO: 15	SEQ. ID NO: 16
Hs.1085	GUCY2C Guanylate cyclase 2C (heat stable enterotoxin receptor)	stomach carcinoma, colon carcinoma	SURFACE, KNOWN TUMOR MARKER	SEQ. ID NO: 17	SEQ. ID NO: 18
Hs.1149	LMO1 LIM domain only 1 (ribonectin 1)	Glioma, retinoblastoma, lung carcinoma tumors, pancreatic insulinoma	KNOWN MARKER FOR LEUKEMIA	SEQ. ID NO: 19	SEQ. ID NO: 20
Hs.1619	ASCL1 Achaete-scute complex-like 1 (Drosophila-like)	neuroblastoma, glioma lung carcinoma tumors, germ cell tumors, kidney tumor, medulloblastoma, ovary tumors	KNOWN TUMOR MARKER	SEQ. ID NO: 21	SEQ. ID NO: 22
Hs.1854	KCN4 Potassium voltage-gated channel, shaker-related subfamily, member 4	lung carcinoma tumors, lung carcinomas	SURFACE	SEQ. ID NO: 23	SEQ. ID NO: 24
Hs.1925	DSG3 Desmoglein 3 (pemphigus vulgaris antigen)	lung carcinomas, pancreatic carcinoma	RARENEOPLASTIC MARKER	SEQ. ID NO: 25	SEQ. ID NO: 26
Hs.2266	CHRNA1 Cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)	Rhabdomyosarcoma	SURFACE	SEQ. ID NO: 27	SEQ. ID NO: 28
Hs.2693	GLI Glioma-associated oncogene homolog (zinc finger protein)	Rhabdomyosarcoma, germ cell tumors, leiomyosarcoma, ovarian tumors, melanoma, Burkitt lymphoma	KNOWN MARKER FOR GLIOMA	SEQ. ID NO: 29	SEQ. ID NO: 30
Hs.2860	POU5F1 POU domain, class 5, transcription factor 1	gastric carcinoma, germ cell tumors, uterus carcinoma, ovarian tumors, teratocarcinoma, lung tumor	KNOWN MARKER FOR GERM CELL TUMORS	SEQ. ID NO: 31	SEQ. ID NO: 32
Hs.2928	SLC7A1 Solute carrier family 7 (cationic amino acid transporter, y-system), member 1	melanoma, glioma, rhabdomyosarcoma neuroblastoma, colon carcinoma, lymphoma	SURFACE	SEQ. ID NO: 33	SEQ. ID NO: 34
Hs.3057	ZNF74 Zinc finger protein 74 (Cos52)	cervical carcinoma, leiomyosarcoma, rhabdomyosarcoma glioma, teratocarcinoma, neuroblastoma, prostate		SEQ. ID NO: 35	SEQ. ID NO: 36

		carcinoma, colon carcinoma, choriocarcinoma, bladder transitional cell papilloma				
Hs. 3104	KIAA0042 (KIAA0042 gene product) POM1	Leiomyosarcoma, testicular cancer, prostate carcinoma, bladder carcinoma, kidney hypernephroma, ovarian tumors, lung carcinoma		SEQ. ID NO: 37		SEQ. ID NO: 38
Hs. 5366	EPSSR3 Epidermal growth factor receptor pathway substrate 8 related protein 3	Colon carcinoma, kidney tumors, germ cell tumors, stomach carcinoma		SEQ. ID NO: 39		SEQ. ID NO: 40
Hs. 6168	KIAA0703 (KIAA0703 gene product) POM2	Pancreatic carcinoma, colon carcinoma, bladder transitional cell papilloma, ovarian carcinoma, breast carcinoma, lung carcinoma		SEQ. ID NO: 41		SEQ. ID NO: 42
Hs. 30743	PRAME Preferentially expressed antigen in melanoma	Brain neuroblastoma, melanoma, lung carcinoma, small intestine carcinoma, retinoblastoma, leiomyosarcoma, uterus carcinoma, choriocarcinoma, kidney carcinoma, ovarian carcinoma, bresat carcinoma, germ cell tumor, esophageal squamous cell carcinoma, colon juvenile granulosa tumor, cervical carcinoma	KNOWN TUMOR MARKER FOR MELANOMA	SEQ. ID NO: 43		SEQ. ID NO: 44
Hs. 30751	LOC55924 Hypothetical protein LOC55924 POM3	Retinoblastoma, rhabdomyosarcoma, prostate carcinoma, Burkitt lymphoma		SEQ. ID NO: 45		SEQ. ID NO: 46
Hs. 36793	SLC12A8 Solute carrier family 12 (potassium/chloride transporters), member 8	Lymphoma, colon, ovarian, stomach, prostate, endometrial and hepatic carcinomas	SURFACE	SEQ. ID NO: 47		SEQ. ID NO: 48
Hs. 37045	PTH Parathyroid hormone	parathyroid tumor	KNOWN TUMOR MARKER	SEQ. ID NO: 49		SEQ. ID NO: 5
Hs. 37107	MAGEA4 Melanoma antigen, family A, 4	intestine duodenal carcinoma, glioma, pharynx squamous cell, uterus, ovarian, melanoma	KNOWN TUMOR MARKER FOR MELANOMA	SEQ. ID NO: 51		SEQ. ID NO: 5
Hs. 37110	MAGEA9 Melanoma antigen, family A, 9	Lung carcinoma, bladder transitional cell papilloma, T cell leukemia, genitourinary tract transitional cell tumors	KNOWN TUMOR MARKER FOR MELANOMA	SEQ. ID NO: 53		SEQ. ID NO: 5
Hs. 46452	SCGB2A2 Secretoglobulin, family 2A, member 2	Lung carcinoma	SURFACE	SEQ. ID NO: 55		SEQ. ID NO: 5
Hs. 48956	GJB6 Gap junction protein, beta 6 (connexin 30)	glioma, prostate carcinoma, uterus carcinoma, pancreatic carcinoma, skin squamous cell carcinoma	SURFACE	SEQ. ID NO: 57		SEQ. ID NO: 5
Hs. 49605	ESTs, Weakly similar to hypothetical protein FLJ22184 [Homo sapiens] POM4	melanoma		SEQ. ID NO: 59		SEQ. ID NO: 6

13563	COL9A3 Collagen, type IX, alpha 3	melanoma, choriocarcinoma, B-cell chronic lymphocytic leukemia, germ cell, uterus serous carcinoma, stomach carcinoma, retinoblastoma, sarcoma, glioma, cervical carcinoma		SEQ. ID NO: 61	SEQ. ID NO: 62
14424	HNFA Hepatocyte nuclear factor 4, alpha	Kidney tumors, germ cell tumors, colon carcinoma		SEQ. ID NO: 63	SEQ. ID NO: 64
1567	PAX1 Paired box gene 1	leiomyosarcoma		SEQ. ID NO: 65	SEQ. ID NO: 66
16357	POM5	Endometrial, pancreatic, lymphoma, lung B-cell chronic lymphocytic leukemia		SEQ. ID NO: 67	SEQ. ID NO: 68
17397	HOXA1 Homeobox A1	melanoma, teratocarcinoma, germ cell tumors, stomach carcinoma, hypernephroma, bladder carcinoma		SEQ. ID NO: 69	SEQ. ID NO: 70
17624	POM6	germ cell tumors		SEQ. ID NO: 73	SEQ. ID NO: 74
18864	Membrane-bound phosphatidic acid-selective phospholipase A1	B-cell chronic lymphocytic leukemia, colon, stomach, pancreatic carcinomas	SURFACE	SEQ. ID NO: 75	SEQ. ID NO: 76
3893	DRD2 Dopamine receptor D2	Lung carcinoma, neuroblastoma, glioma, pancreas carcinoma, rhabdomyosarcoma	SURFACE	SEQ. ID NO: 77	SEQ. ID NO: 78
3952	PRH2 Proline-rich protein HaeIII subfamily 2	Nervous tumors, colon carcinoma, head and neck squamous cell carcinoma	SECRETED	SEQ. ID NO: 79	SEQ. ID NO: 80
4126	FABP6 Fatty acid binding protein 6, ileal/gastrointestinal	Lymphoma, uterus carcinoma, kidney carcinoma, lung carcinoma, ovarian carcinoma, lung carcinoma		SEQ. ID NO: 81	SEQ. ID NO: 82
9414	PDEF Prostate epithelium-specific Ets transcription factor	Pancreatic, colon, endometrial, breast, lung, ovarian, stomach, prostate carcinomas and glioma	KNOWN MARKER-BREAST CARCINOMA POSSIBLY PROSTATIC CARCINOMA	SEQ. ID NO: 83	SEQ. ID NO: 84
6232	GDF3 Growth differentiation factor 3	germ cell tumors, neuroepithelial tumors	Embryonal carcinoma stem cell-associated marker; Possibly GERM CELL TUMORS	SEQ. ID NO: 85	SEQ. ID NO: 86
7225	CTAG2 Cancer/testis antigen 2	choriocarcinoma, breast carcinoma, endometrium carcinoma, melanoma, stomach carcinoma	KNOWN TUMOR MARKER	SEQ. ID NO: 87	SEQ. ID NO: 88
9143	POM7	ovarian tumors		SEQ. ID NO: 89	SEQ. ID NO: 90
9605	CHRNA3 Cholinergic receptor, nicotinic, alpha polypeptide3	neuroblastoma, lung carcinoma, small intestine carcinoma	SURFACE	SEQ. ID NO: 91	SEQ. ID NO: 92
17258	POM8 similar to S29539 ribosomal protein 113a, cytosolic	Pancreas, endometrial, ovarian carcinomas, lung carcinoma and germ cell tumors		SEQ. ID NO: 93	SEQ. ID NO: 94
7283	POM9	ovarian tumors		SEQ. ID NO: 95	SEQ. ID NO: 96
7860	KIRAL484 KIRAL484 protein	Ovarian carcinoma, retinoblastoma, endometrium carcinoma		SEQ. ID NO: 97	SEQ. ID NO: 98

Hs.98988	POM10 Homo sapiens, clone IMAGE:4425111.mRNA, partial cds	germ cell tumors, hypernephroma, ovarian tumors, colon, uterus, stomach, pancreas, skin squamous cell carcinomas	SEQ. ID NO: 99	SEQ. ID NO: 100
Hs.99624	POM11	parathyroid tumor, ovarian tumor, Stomach carcinoma	SEQ. ID NO: 101	SEQ. ID NO: 102
Hs.99960	NG4A3 Membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific)	lung carcinoma, chronic myelogenous leukemia, prostate carcinoma	SEQ. ID NO: 103	SEQ. ID NO: 104
Hs.103504	ESR2 Estrogen receptor 2 (ER beta)	germ cell tumors, lung carcinoma, neuroblastoma	SEQ. ID NO: 105	SEQ. ID NO: 106
Hs.103707	MUC5AC Mucin 5, subtypes A and C, tracheobronchial/gastric	COLON, PANCREATIC, STOMACH CARCINOMAS, LUNG TUMORS	SEQ. ID NO: 107	SEQ. ID NO: 108
Hs.104073	POM12	Colon, stomach carcinoma	SEQ. ID NO: 109	SEQ. ID NO: 110
Hs.104115	ZNFI0 Zinc finger protein 10 (K0X1)	parathyroid, lung carcinoma, nervous cell tumors, adrenal cortex carcinoma, germ cell tumors, uterus tumor, multiple myeloma	SEQ. ID NO: 111	SEQ. ID NO: 112
Hs.105484	REG-IV Regenerating gene type IV	Prostate, duodenal, colon and stomach carcinomas, B-cell chronic lymphocytic leukemia, acute myelogenous leukemia	SEQ. ID NO: 113	SEQ. ID NO: 114
Hs.105667	POM13	ovarian tumors	SEQ. ID NO: 115	SEQ. ID NO: 116
Hs.105924	DEFB4 Defensin, beta 4	Head and neck carcinoma	SEQ. ID NO: 117	SEQ. ID NO: 118
Hs.112341	PI3 Protease inhibitor 3, skin-derived (SKALP)	Glioma, B-cell chronic lymphocytic leukemia, uterus, lung and colon carcinomas, ovarian, prostate, colon carcinomas, bladder, nervous cell and placenta tumors	SEQ. ID NO: 119	SEQ. ID NO: 120
Hs.113262	HTR45 hydroxytryptamine (serotonin) receptor 4	Schwannoma	SEQ. ID NO: 121	SEQ. ID NO: 122
Hs.114905	ERN2 (ER to nucleus signalling 2)	Stomach, colon, pancreatic carcinoma	SEQ. ID NO: 123	SEQ. ID NO: 124
Hs.117938	COL17A1 Collagen, type XVII, alpha 1	glioma, pancreas, lung, colon, nasopharyngeal, stomach carcinomas, germ cell, bladder, uterus tumors, leiomyosarcoma	SEQ. ID NO: 125	SEQ. ID NO: 126
Hs.122310	POM14	parathyroid tumor	SEQ. ID NO: 127	SEQ. ID NO: 128
Hs.123094	SAL11 Sal-like 1 (Drosophila)	Retinoblastoma, germ cell tumors, glioma	SEQ. ID NO: 129	SEQ. ID NO: 130
Hs.123993	POM15	Glioma, colon carcinoma, lung carcinoma tumors, parathyroid tumor	SEQ. ID NO: 131	SEQ. ID NO: 132
Hs.124173	POM16	Weakly similar to T00366 hypothetical protein KIAA0669	SEQ. ID NO: 133	SEQ. ID NO: 134
Hs.124638	POM17	parathyroid tumor	SEQ. ID NO: 135	SEQ. ID NO: 136
		COLON CARCINOMA	SEQ. ID NO: 137	

				SEQ. ID NO: 138	SEQ. ID NO: 139
Hs.125293	POM18	Glioma, lung carcinoma, kidney tumors, germ cell tumors, parathyroid tumor, stomach carcinoma, ovary carcinoma			
Hs.126566	POM19	Colon carcinoma		SEQ. ID NO: 140	SEQ. ID NO: 141
Hs.126869	POM20	LUNG CARCINOID TUMORS, germ cell tumor		SEQ. ID NO: 142	SEQ. ID NO: 143
Hs.127144	POM21	Colon carcinoma		SEQ. ID NO: 144	SEQ. ID NO: 145
Hs.127383	POM22	Colon carcinoma		SEQ. ID NO: 146	SEQ. ID NO: 147
Hs.127476	POM23	Lung carcinoid tumors, glioma, kidney tumors, chondrosarcoma, germ cell tumors, Ewing's sarcoma		SEQ. ID NO: 148	SEQ. ID NO: 149
	Highly similar to BTG2_HUMAN BTG2 PROTEIN PRECURSOR				
Hs.128001	POM24	COLON CARCINOMA		SEQ. ID NO: 150	SEQ. ID NO: 151
Hs.128115	POM25 Homo sapiens cDNA FLJ32217 fls, clone PLACE6003771	germ cell, lung carcinoid and kidney tumors, glioma, melanoma		SEQ. ID NO: 153	SEQ. ID NO: 154
Hs.128326	POM26	germ cell tumors		SEQ. ID NO: 155	SEQ. ID NO: 156
Hs.128398	POM27	Lung carcinoid tumors		SEQ. ID NO: 157	
Hs.128436	POM28, Moderately similar to putative secreted protein [Homo sapiens]	Lung carcinoid tumors		SEQ. ID NO: 158	SEQ. ID NO: 159
Hs.128437	POM29, Weakly similar to S33477 hypothetical protein l - rat	Lung carcinoid tumors, kidney tumors, cervical carcinoma		SEQ. ID NO: 160	SEQ. ID NO: 161
Hs.128907	POM30, Weakly similar to orthopedia homolog (Drosophila); orthopedia (Drosophila) homolog; orthopedia (Drosophila) homolog; Orthopedia, homolog of Drosophila gene [Homo sapiens] [H.sapiens]	LUNG CARCINOID TUMORS		SEQ. ID NO: 162	SEQ. ID NO: 163
Hs.129040	POM31	parathyroid tumor, lung carcinoid tumors		SEQ. ID NO: 164	SEQ. ID NO: 1
Hs.129108	POM32	Lung carcinoid tumors		SEQ. ID NO: 166	SEQ. ID NO: 1
	clone IMAGE:2337282				
Hs.129302	POM33	lung carcinoma, germ cell tumors		SEQ. ID NO: 168	SEQ. ID NO: 1
Hs.129782	MUC3B Mucin 3B	Pancreatic carcinoma, kidney tumors, colon carcinoma chorioncarcinoma, breast carcinoma, stomach tumor, head and neck tumor, lung tumor, ovary tumor	PROBABLY KNOWN TUMOR MARKER	SEQ. ID NO: 170	SEQ. ID NO: 1
Hs.131358	POM34	germ cell tumors, choriocarcinoma		SEQ. ID NO: 172	SEQ. ID NO: 1
Hs.132370	NOX1 NADPH oxidase 1	colon carcinomas, glioma, lung carcinoid tumors, kidney tumors, breast carcinoma		SEQ. ID NO: 174	SEQ. ID NO: 1
Hs.132576	Paired box gene 9	Lung carcinoma, parathyroid tumor, stomach carcinoma , head and neck carcinoma		SEQ. ID NO: 176	SEQ. ID NO: 1
				SEQ. ID NO: 178	SEQ. ID NO: 1

Hs.133081	POM35 Homo sapiens cDNA FLJ25124 fis	Esophagus carcinoma, germ cell tumors, glioma, lung carcinoma, chondrosarcoma, uterus carcinoma	SEQ. ID NO: 180	SEQ. ID NO: 181
Hs.133089	DFFB DNA fragmentation factor, 40 kD, beta polypeptide (caspase-activated DNase)	lung carcinoma, breast carcinoma, colon carcinoma, nervous cell tumor, leiomyoma, acute myelogenous leukemia, osteosarcoma	SEQ. ID NO: 182	SEQ. ID NO: 183
Hs.133107	POM36	Ovary carcinoma, lung carcinoma, glioma	SEQ. ID NO: 184	SEQ. ID NO: 185
Hs.133294	POM37	Uterus carcinoma, lung carcinoma, Ovary carcinoma, chronic myelogenous leukemia, breast carcinoma, glioma, colon juvenile granulosa tumor, adrenal adenoma, prostate tumor, head and neck carcinoma	SEQ. ID NO: 186	SEQ. ID NO: 187 SEQ. ID NO: 188
Hs.133296	POM38	Ovary carcinoma, lung carcinoma	SEQ. ID NO: 189	SEQ. ID NO: 190
Hs.133300	POM39	Breast carcinoma, ovary carcinoma, lung carcinoma	SEQ. ID NO: 191	SEQ. ID NO: 192
Hs.133451	POM40	germ cell tumors, colon carcinoma	SEQ. ID NO: 193	SEQ. ID NO: 194
Hs.135365	POM41	Pancreatic carcinoma, ovarian carcinoma, lung carcinoma	SEQ. ID NO: 195	SEQ. ID NO: 196
Hs.140457	POM42	Kidney tumors, lung carcinoma, glioma, cervical carcinoma, stomach tumors	SEQ. ID NO: 197	SEQ. ID NO: 198
Hs.142907	POM43 Human BRCA2 region, mRNA sequence CG011	Lung carcinoma, fibrotheoma, ovary tumors, uterus tumors	SEQ. ID NO: 199	SEQ. ID NO: 200
Hs.143507	T T, brachyury homolog	Lung carcinoma, B-cell chronic lymphocytic leukemia, breast carcinoma, germ cell tumors	SEQ. ID NO: 201	SEQ. ID NO: 202
Hs.143949	POM44	Colon carcinoma	SEQ. ID NO: 203	SEQ. ID NO: 2
Hs.144063	POM45	Lung carcinoma	SEQ. ID NO: 205	SEQ. ID NO: 2
Hs.144121	POM46, Moderately similar to hypothetical protein, MNCb-123; hypothetical protein, MNCb-1231	glioma, lung carcinoma	SEQ. ID NO: 207	SEQ. ID NO: 2
Hs.145327	POM47	Chronic myelogenous leukemia, Ovary carcinoma, colon carcinoma, lung carcinoma, head and neck carcinoma	SEQ. ID NO: 209	SEQ. ID NO: 2
Hs.145340	POM48	lung carcinoma, Ovary carcinoma, head and neck carcinoma	SEQ. ID NO: 211	SEQ. ID NO: 2
Hs.145356	POM49	Ovary carcinoma, lung carcinoma	SEQ. ID NO: 213	SEQ. ID NO: 2
Hs.145357	POM50	Ovary carcinoma, breast carcinoma, head and neck carcinoma, lung carcinoma	SEQ. ID NO: 215	SEQ. ID NO: 2
Hs.145489	POM51	Ovary carcinoma	SEQ. ID NO: 217	SEQ. ID NO: 2

Hs.145492	POM52	Ovary carcinoma, lung carcinoma	SEQ. ID NO: 219	SEQ. ID NO: 220
Hs.145493	POM53	Ovary carcinoma, uterus tumor	SEQ. ID NO: 221	SEQ. ID NO: 222
Hs.145500	POM54	Ovary carcinoma, lung carcinoma	SEQ. ID NO: 223	SEQ. ID NO: 224
Hs.145509	POM55	Lung carcinoma, ovary carcinoma, breast carcinoma, glioma, stomach carcinoma	SEQ. ID NO: 225	SEQ. ID NO: 226
Hs.145661	POM56	Colon carcinoma	SEQ. ID NO: 227	SEQ. ID NO: 228
Hs.145809	POM57, Weakly similar to T31613 hypothetical protein Y5088A.1 - <i>Caenorhabditis elegans</i>	Uterus carcinoma, stomach carcinoma, pancreatic carcinoma, placenta tumor	SEQ. ID NO: 229	
Hs.146200	POM58	Ovary carcinoma, breast carcinoma, head and neck carcinoma	SEQ. ID NO: 230	SEQ. ID NO: 231
Hs.147291	POM59	germ cell tumors	SEQ. ID NO: 232	SEQ. ID NO: 233
Hs.148661	POM60	Lung carcinoma tumors, germ cell tumors	SEQ. ID NO: 234	SEQ. ID NO: 235
Hs.152290	POM61, Highly similar to VIPS HUMAN VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR [H.sapiens]	Rhabdomyosarcoma, glioma, colon carcinoma	SEQ. ID NO: 236	SEQ. ID NO: 237
Hs.152531	HAND1 Heart and neural crest derivatives expressed 1	Neuroblastoma, Schwannoma, germ cell tumors, sarcoma	SEQ. ID NO: 238	SEQ. ID NO: 239
Hs.153444	POM62	Lung carcinoma tumors, breast carcinoma	SEQ. ID NO: 240	SEQ. ID NO: 241
Hs.352562	POM63, Homo sapiens cDNA FLJ33010 fls, clone TRIM01000336 UniGene cluster identifier Hs.154173 has been retired	Teratocarcinoma, liposarcoma, pheochromocytoma, lung carcinoma, cervical carcinoma, chondrosarcoma, breast carcinoma, leiomyoma, lymphoma, uterus tumor, head and neck carcinoma, colon carcinoma, breast carcinoma, melanoma, skin carcinoma, prostate tumor	SEQ. ID NO: 242	SEQ. ID NO: 243
Hs.155981	current cluster Hs.352562 MSIN Mesothelin	Pancreas, prostate, cervical, liver, uterus, colon, stomach, head and neck and lung carcinomas, choriocarcinoma, glioma, ovarian and uterus tumors, chondrosarcoma	SEQ. ID NO: 244	SEQ. ID NO: 2
Hs.156213	POM64	Lung carcinoma tumors, head and neck carcinoma, colon carcinoma	SEQ. ID NO: 246	SEQ. ID NO: 2
Hs.156499	POM65	Uterus tumors, lymphomas and leukemias	SEQ. ID NO: 248	SEQ. ID NO: 2
Hs.156637	CBLC Cas-Br-M (murine) ectropic retroviral transforming sequence c	stomach, lung, breast, colon, lung pancreas and head and neck carcinomas, glioma, choriocarcinoma Uterus and carcinoma tumors	SEQ. ID NO: 250	SEQ. ID NO: 2
Hs.156762	POM66	germ cell tumors	SEQ. ID NO: 252	SEQ. ID NO: 2
Hs.156810	POM67 Weakly similar to EF11 HUMAN ELONGATION FACTOR 1-ALPHA 1 [H.sapiens]	Uterus carcinoma	SEQ. ID NO: 254	SEQ. ID NO: 2
Hs.156813	POM68 (MGC10600) Predicted protein MGC10600	Melanoma, choriocarcinoma, germ cell tumor	SEQ. ID NO: 256	SEQ. ID NO: 2

Hs.156843	POM69	Lung carcinoid tumors, germ cell tumors, melanoma	SEQ. ID NO: 258	SEQ. ID NO: 259
Hs.156905	KIAA1676	germ cell and lung carcinoid tumors, Ewing's sarcoma, ovary, adrenal cortex and uterus carcinomas, retinoblastoma	SEQ. ID NO: 260	SEQ. ID NO: 261
Hs.157205	BCAT1 Branched chain aminotransferase 1, cytosolic	germ cell tumors, lung carcinoma, glioma, lymphoma, teratocarcinoma, rhabdomyosarcoma, lung carcinoma, embryonal carcinoma, uterus tumor	SEQ. ID NO: 262	SEQ. ID NO: 263
Hs. 79707	TNFRSF19L Tumor necrosis factor receptor superfamily, member 19-like UniGene cluster identifier Hs.158218 has been retired now Hs.79707	Colon carcinoma, glioma, B-cell chronic lymphocytic leukemia, ovary tumors, germ cell tumors, chondrosarcoma, neuroblastoma, melanoma, stomach carcinoma, leiomyosarcoma, renal cell carcinoma, uterus carcinoma, lung carcinoma, lymphoma, pre-B cell acute lymphoblastic leukemia	SEQ. ID NO: 264	SEQ. ID NO: 265
Hs.158333	PRSS7 Protease, serine, 7 (enterokinase)	Glioma, breast carcinoma	SEQ. ID NO: 266	SEQ. ID NO: 267
Hs.158460	CDK5R2 Cyclin-dependent kinase 5, regulatory subunit 2 (p39)	germ cell tumors, lung carcinoid tumors, glioma, adrenal cortex carcinoma, lung carcinoma, neuroblastoma	SEQ. ID NO: 268	SEQ. ID NO: 269
Hs.158521	POM70	Kidney tumors, breast carcinoma	SEQ. ID NO: 270	SEQ. ID NO: 271
Hs.160724	POM71	glioma, lung carcinoid tumors	SEQ. ID NO: 272	SEQ. ID NO: 273
Hs.162717	POM72 (MGC15668) Hypothetical protein	Choriocarcinoma, neuroblastoma, placenta tumor, lung, colon, stomach carcinomas	SEQ. ID NO: 274	SEQ. ID NO: 275
	MGC15668	germ cell tumors, burkitt lymphoma,		

Hs. 236510	TPARL TPA regulated locus	Melanoma, rhabdomyosarcoma, renal cell carcinoma, mucoepidermoid carcinoma, uterus carcinoma, B-cell chronic lymphocytic leukemia, colon carcinoma, lymphoma, ovary fibrotheoma, lung carcinoma, kidney tumors, breast carcinoma, glioma, parathyroid tumor, germ cell tumors, liposarcoma, thyroid tumor, lung carcinoid tumors, liposarcoma, small intestine duodenal carcinoma, genitourinary tract transitional cell tumors, head and neck carcinoma, melanoma, endometrium carcinoma, adrenal cortex carcinoma, osteosarcoma, oral carcinoma, synovial sarcoma, lung carcinoma, renal cell carcinoma, chondrosarcoma, breast carcinoma, melanoma, meningioma, lymphoma, chronic myelogenous leukemia, embryonal cell carcinoma	SEQ. ID NO: 276	SEQ. ID NO: 277
Hs. 356072	POM73, Moderately similar to POL2 HUMAN RETROVIRUS-RELATED POLYPROTEIN [H.sapiens]	lung carcinoid tumors, lung carcinoma	SEQ. ID NO: 278	SEQ. ID NO: 279
Hs. 336963	EVX1 Eve, even-skipped homeo box homolog 1 (Drosophila)	Colon carcinoma	SEQ. ID NO: 280	SEQ. ID NO: 281
Hs. 170046	POM74	Ovary carcinoma	SEQ. ID NO: 282	SEQ. ID NO: 283
Hs. 170482	MYL5 Myosin, light polypeptide 5, regulatory	Ovary tumors, glioma, lung carcinoma, breast colon and pancreatic carcinoma, kidney tumors, leiomyosarcoma, uterus tumors	SEQ. ID NO: 284	SEQ. ID NO: 285
Hs. 170993	POM75	Kidney tumors, prostatic carcinoma	SEQ. ID NO: 286	SEQ. ID NO: 2
Hs. 172330	POM76 (MGC2705) predicted MGC2705	cervical, lung and breast carcinoma, retinoblastoma, melanoma, leiomyosarcoma, Wilms tumor, breast rhabdomyosarcoma, acute myelogenous leukemia, burkitt lymphoma	SEQ. ID NO: 288	SEQ. ID NO: 2
Hs. 172603	POM77	prostate carcinoma	SEQ. ID NO: 290	SEQ. ID NO: 2
Hs. 330485	POM78	Ovary carcinoma	SEQ. ID NO: 292	SEQ. ID NO: 2
Hs. 180142	CLSP Calmodulin-like skin protein	Skin carcinoma, breast carcinoma, lung carcinoma	SEQ. ID NO: 294	SEQ. ID NO: 2
Hs. 328801	POM79	lung carcinoma, breast carcinoma	SEQ. ID NO: 296	SEQ. ID NO: 2
Hs. 181654	POM80	lung carcinoid tumors, kidney tumors	SEQ. ID NO: 298	SEQ. ID NO: 2
Hs. 182362	POM90	ovarian carcinoma, kidney tumors	SEQ. ID NO: 300	SEQ. ID NO: 3
Hs. 185831	POM91	Prostate, stomach and bladder carcinoma	SEQ. ID NO: 302	SEQ. ID NO: 3
Hs. 189358	POM92	lung carcinoid tumors, germ cell tumors, breast carcinoma	SEQ. ID NO: 304	SEQ. ID NO: 3

Hs.190488	POM93 (Homo sapiens mRNA; cDNA DXFZp667M2411 (from clone DXFZp667M2411))	Skin squamous cell carcinoma, stomach carcinoma, colon carcinoma, parathyroid tumor, lung carcinoid tumors, glioma, breast carcinoma, lymphoma, melanoma, uterus carcinoma, prostate carcinoma, chondrosarcoma, retinoblastoma, cervical carcinoma, renal carcinoma, head and neck carcinoma, chronic myelogenous leukemia, hypernephroma, uterus carcinoma, leiomyoma	SEQ. ID NO: 306	SEQ. ID NO: 307
Hs.191574	POM94 (Homo sapiens cDNA FLJ13050 fis, clone NT2R33001432)	Pancreas carcinoma, parathyroid tumor, ovary tumors, teratocarcinoma, acute myelogenous leukemia, lung carcinoid tumors, hypernephroma, head and neck carcinoma, melanoma	SEQ. ID NO: 308	SEQ. ID NO: 309
Hs.193677	ZNF141 Zinc finger protein 141 (clone PHZ-44)	Retinoblastoma, lung carcinoid tumors, hypernephroma, glioma, head and neck carcinoma ovary tumors, leiomyoma	SEQ. ID NO: 310	SEQ. ID NO: 311
Hs.195081	POM95	germ cell tumors	SEQ. ID NO: 312	SEQ. ID NO: 313
Hs.195374	POM96	germ cell tumors, B-cell chronic lymphocytic leukemia, kidney tumor, uterus tumors	SEQ. ID NO: 314	SEQ. ID NO: 315
Hs.195641	POM97	uterus carcinoma, lung carcinoma, colon carcinoma, nervous cell tumors, breast carcinoma, stomach carcinoma	SEQ. ID NO: 316	SEQ. ID NO: 317
Hs.196073	POM98	lung carcinoma, germ cell tumors, stomach carcinoma, genitourinary tract transitional cell carcinoma	SEQ. ID NO: 318	SEQ. ID NO: 3
Hs.199460	DPCL1 DPCL1 protein	Pancreas carcinoma, stomach carcinoma	SEQ. ID NO: 320	SEQ. ID NO: 3
Hs.202247	POM99	lung carcinoid tumors	SEQ. ID NO: 322	SEQ. ID NO: 3
Hs.202512	POM100	lung carcinoid tumors, colon carcinoma	SEQ. ID NO: 324	SEQ. ID NO: 3
Hs.202577	POM101 (Homo sapiens cDNA FLJ12166 fis, clone MAMWA1000616)	Schwannoma, lung carcinoid tumors, germ cell tumors, lymphoma, colon carcinoma, glioma	SEQ. ID NO: 326	SEQ. ID NO: 3
Hs.202612	POM102	lung carcinoma, colon carcinoma	SEQ. ID NO: 328	SEQ. ID NO: 3
Hs.209560	POM103	lung carcinoma, embryonal cell carcinoma, pituitary tumor	SEQ. ID NO: 330	SEQ. ID NO: 3
Hs.209646	POM104 (K1A1118) K1A1118 protein	lung carcinoma, choriocarcinoma, melanoma, glioblastoma, neuroblastoma, osteosarcoma, colon carcinoma, breast carcinoma, lymphoma, glioma, retinoblastoma	SEQ. ID NO: 332	SEQ. ID NO: 3
Hs.211238	IL-1HI Interleukin-1 homolog 1	colon carcinoma, head and neck carcinoma	SEQ. ID NO: 334	SEQ. ID NO: 3

Hs.217766	POM105	Ovary carcinoma		SEQ. ID NO: 336	SEQ. ID NO: 337
Hs.217882	POM106	glioma, colon carcinoma, kidney tumors, prostate tumors, lung carcinoma, hypernephroma, head and neck carcinoma, duodenal carcinoma, melanoma, pancreatic carcinoma, uterus tumors		SEQ. ID NO: 338	SEQ. ID NO: 339
Hs.220529	CEACAM5 Carcinoembryonic antigen-related cell adhesion molecule 5	Pancreas carcinoma, colon carcinoma, stomach carcinoma, head and neck carcinoma, lung carcinoma leiomioma, breast carcinoma	KNOWN TUMOR MARKER	SEQ. ID NO: 340	SEQ. ID NO: 341
Hs.222056	POM107 Homo sapiens cDNA FLJ11572 fis, clone HEMBA1003373	Stomach carcinoma, head and neck carcinoma, breast carcinoma		SEQ. ID NO: 342	SEQ. ID NO: 343
Hs.225083	POM108	Melanoma, ovary tumors, colon carcinoma, parathyroid tumor, kidney tumors, head and neck carcinoma		SEQ. ID NO: 344	SEQ. ID NO: 345
Hs.227098	GCMB Glial cells missing homolog b (Drosophila)	parathyroid tumor		SEQ. ID NO: 346	SEQ. ID NO: 347
Hs.239107	POM109	Lymphoma, germ cell tumors, head and neck carcinoma		SEQ. ID NO: 348	SEQ. ID NO: 349
Hs.239891	GPR35 G protein-coupled receptor 35	B-cell chronic lymphocytic leukemia, colon carcinoma, pancreas and carcinoma	SURFACE	SEQ. ID NO: 350	SEQ. ID NO: 351
Hs.241381	CRSP7 Cofactor required for Sp1 transcriptional activation, subunit 7 (70kd)	Pancreatic carcinoma, duodenal carcinoma, ovary carcinoma, melanoma, osteosarcoma, glioma, leiomyosarcoma, germ cell tumors		SEQ. ID NO: 352	SEQ. ID NO: 353
Hs.241407	SERPINB13 Serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13	ORAL carcinoma, cervical carcinoma, head and neck carcinoma		SEQ. ID NO: 354	SEQ. ID NO: 355
Hs.243920	POM110	Pancreas carcinoma		SEQ. ID NO: 356	SEQ. ID NO: 357
Hs.244378	SLC2A6 Solute carrier family 2 (facilitated glucose transporter), member 6	Hypernephroma, pancreatic carcinoma, glioma, lung carcinoma, neuroblastoma, renal cell carcinoma, adrenal gland tumors		SEQ. ID NO: 358	SEQ. ID NO: 359
Hs.246781	POM111	parathyroid tumor, lung carcinoma tumors, germ cell tumors, hepatocellular carcinoma, stomach carcinoma, breast carcinoma		SEQ. ID NO: 360	SEQ. ID NO: 361

Hs.247817	H2B/S Histone family member A	Breast carcinoma, chronic myelogenous leukemia, cervical carcinoma, melanoma, ovary carcinoma, lung carcinoma, osteosarcoma, mucopidermoid carcinoma, duodenal carcinoma, leiomyosarcoma, glioma, prostate carcinoma, kidney tumors, colon carcinoma, prostatic intraepithelial neoplasia, lymphoma, uterus carcinoma, parathyroid tumor, insulinoma, chondrosarcoma, ovary tumors, multiple myeloma, chondrosarcoma, bladder tumors, parathyroid tumors, insulinoma, breast carcinoma, pnet tumors,	SEQ. ID NO: 362	SEQ. ID NO: 363
Hs.250158	POM12	Head and neck carcinoma, stomach carcinoma, colon carcinoma	SEQ. ID NO: 364	SEQ. ID NO: 365
Hs.250848	Pom13Homo sapiens cDNA FLJ14761 f1s, clone NT2R33003302	Uterus carcinoma, prostate tumor, glioma, duodenal carcinoma, colon carcinoma, glioma, stomach carcinoma, Germ cell tumors, lung carcinoma, embryonal cell carcinoma, breast carcinoma, choriocarcinoma	SEQ. ID NO: 366	SEQ. ID NO: 367
Hs.252351	HHLA2 HERV-H LTR-associating 2	Colon carcinoma, kidney tumors, ovary tumors, Stomach tumors, prostate carcinoma,	SEQ. ID NO: 368	SEQ. ID NO: 369
Hs.253298	POM14	Head and neck carcinoma, germ cell tumors	SEQ. ID NO: 370	SEQ. ID NO: 371
Hs.254379	POM15	Ovary carcinoma	SEQ. ID NO: 372	SEQ. ID NO: 373
Hs.255877	POM16	Leukemia	SEQ. ID NO: 374	SEQ. ID NO: 375
Hs.266390	POM17	Lung carcinoma tumors, pre-B cell acute lymphoblastic leukemia, ovarian carcinoma	SEQ. ID NO: 376	SEQ. ID NO: 377
Hs.268171	POM18	Nervous cell tumors, germ cell tumors, prostatic intraepithelial neoplasia, ovary tumors	SEQ. ID NO: 378	SEQ. ID NO: 379

Hs. 106823	STX12 Syntaxin 12 and MGC14797 Hypothetical protein MGC14797	Bladder carcinoma, colon carcinoma, lymphoma, prostate carcinoma, pancreas carcinoma, breast carcinoma, Wilms' tumor, uterus carcinoma, meningioma, kidney tumors, lung carcinoma, stomach carcinoma, parathyroid tumor, germ cell tumors, ovary tumors, B-cell chronic lymphocytic leukemia, germ cell tumors, thyroid tumor, leiomyosarcoma, duodenal carcinoma, pancreatic carcinoma, alveolar rhabdomyosarcoma, glioma, head and neck carcinoma, bladder transitional cell papilloma, retinoblastoma, chondrosarcoma, stomach carcinoma, pre-B cell acute lymphoblastic leukemia, lung carcinoma, hepatocellular carcinoma, melanoma, fibrosarcoma, lymphoma, chondrosarcoma, osteosarcoma, hepatocellular carcinoma, burkitt lymphoma, uterus carcinoma	SEQ. ID NO: 380 SEQ. ID NO: 382	SEQ. ID NO: 381 SEQ. ID NO: 383
Hs.365428	Pom119, Weakly similar to B34087 Predicted protein [H.sapiens]	Pancreas carcinoma, glioma, breast carcinoma, lung carcinoid tumors, Ewing's sarcoma, colon carcinoma, melanoma, lung carcinoma, head and neck carcinomas, ovary carcinoma, pnet tumor	SEQ. ID NO: 384	SEQ. ID NO: 3
Hs.272216	GP6 Glycoprotein VI (platelet)	Rhabdomyosarcoma, colon carcinoma, head and neck carcinoma, epidydimal tumors, nervous cell tumors	SEQ. ID NO: 386	SEQ. ID NO: 3
Hs.272499	DHRS2 Dehydrogenase/reductase (SDR family) member 2	Bladder transitional cell papilloma, melanoma, colon carcinoma, hepatocellular carcinoma, endometrial carcinoma, lung carcinoid tumors, colon carcinoma, lymphoma, fibrosarcoma, kidney tumor, meningioma, genitourinary tract transitional cell tumors, fibrosarcoma, stomach tumor, breast carcinoma,	SEQ. ID NO: 388	SEQ. ID NO: 3
Hs.273625	POM120	Stomach carcinoma	SEQ. ID NO: 390	SEQ. ID NO: 3

Hs.278291	POM121 Weakly similar to 810024J URF 4 [H.sapiens]	endometrial carcinoma	SEQ. ID NO: 392	SEQ. ID NO: 393
Hs.279805	POM122	Lung carcinoid tumors, nervous cell tumors, pnet tumor,	SEQ. ID NO: 394	
Hs.280146	POM123 Weakly similar to l1 repeat, Tf subfamily, member 18 [Mus musculus]	Lung carcinoid and ovarian tumors, glioma	SEQ. ID NO: 395	
Hs. 109274	POM124 MGC4365 Predicted protein MGC4365	Lung carcinoma, stomach carcinoma, colon carcinoma, breast carcinoma, glioma, kidney tumors, melanoma, choriocarcinoma, t-cell leukemia, cervical carcinoma, neuroblastoma, retinoblastoma, multiple myeloma, ovary carcinoma, pre-B-cell acute lymphoblastic leukemia, uterus carcinoma, kidney tumors, lung carcinoma, endometrial carcinoma, renal cell carcinoma, acute myelogenous leukemia cell, cervical carcinoma	SEQ. ID NO: 396	SEQ. ID NO: 397
Hs.282050	POM125 Homo sapiens cDNA FLJ31265 fis, clone KIDNE2006030, moderately similar to Gallus gallus syndesmos mRNA	Prostate carcinoma, embryonal cell carcinoma, ovary carcinoma, kidney tumors, colon carcinoma, germ cell tumors, neuroblastoma, retinoblastoma, melanoma, breast carcinoma, ovary tumors, renal cell carcinoma, endometrium carcinoma, leiomyosarcoma, glioma, head and neck carcinoma, nervous cell tumors, neuroblastoma, cervical carcinoma, leukemia, ovarian carcinoma, head and neck tumors.	SEQ. ID NO: 398	SEQ. ID NO: 399
Hs.284203	MYO1 Myogenic factor 3	Rhabdomyosarcoma, burkitt lymphoma	SEQ. ID NO: 400	SEQ. ID NO: 4
Hs.285026	HHLA1 HERV-H ITR-associating 1	Colon carcinoma	SEQ. ID NO: 402	SEQ. ID NO: 4
Hs.285887	POM126 Weakly similar to 2109260A B cell growth factor [H.sapiens]	hepatocellular carcinoma	SEQ. ID NO: 404	SEQ. ID NO: 4
Hs.285894	POM127	hepatocellular carcinoma	SEQ. ID NO: 406	SEQ. ID NO: 4
Hs.288568	POM128 FLJ22644 Predicted protein FLJ22644	Stomach carcinoma	SEQ. ID NO: 408	SEQ. ID NO: 4

Hs.288842	OPA3 Optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia)	Lymphoma, kidney renal cell carcinoma, lung small cell carcinoma, pancreas carcinoma, choriocarcinoma, Melanoma, retinoblastoma, leiomyosarcoma, prostate carcinoma, head and neck carcinoma, parathyroid tumor, choriocarcinoma	SEQ. ID NO: 410	SEQ. ID NO: 411
Hs.290308	POM129	ovarian carcinoma, glioma, hepatocellular carcinoma, breast carcinoma, head and neck carcinoma, insulinoma, retinoblastoma	SEQ. ID NO: 412	SEQ. ID NO: 413
Hs.293678	TCHAP0758 Predicted protein TCHAP0758	Retinoblastoma, leiomyosarcoma, lymphoma, neuroblastoma, glioma, cervical carcinoma, pancreas carcinoma, germ cell tumors, stomach carcinoma, glioma, uterus carcinoma, lung carcinoma tumors, adrenal cortex carcinoma, ovary tumors, melanoma, lymphoblastic leukemia, colon cancer, endometrial carcinoma, neuroblastoma, breast carcinoma, head and neck neck carcinoma, nervous cell tumors, lung carcinoma, Wilms' tumor, pancreas carcinoma	SEQ. ID NO: 414	SEQ. ID NO: 4

[000102] Of the tumor associated EST's detected by the methods of the present invention, a particularly interesting group are the clusters represented by EST's found exclusively in tumor derived libraries. One striking feature of these tumor markers is their frequent occurrence in colon, lung and ovarian carcinomas. Thus, the high percentage of tumor-specific EST's is characteristic of highly malignant tumors (e.g. ovary carcinomas, metastatic breast carcinomas and small cell lung tumors. Accordingly, the methods of the present invention provide a method for predicting malignancy of a tumor based on the percentage of tumor-specific EST expression detected in such tumors. Utilizing standard molecular biology techniques as exemplified below, for example, persons of ordinary skill in the art can utilize probes for tumor associated EST's to determine the level of malignancy in a tumor tissue sample.

[000103] All three colon-specific clusters detected with the methods of the present invention represented known genes which encode apolipoprotein B mRNA editing protein APOBEC1, guanylate cyclase 2C and G protein coupled receptor 35. Both APOBEC1 and guanylate cyclase 2C mRNAs have been shown to be overexpressed in colon carcinomas (Lee et al, Gastroenterology 115(5):1096-1103 (1998); Carithers et al. Proc.Natl. Acad. Sci. USA 93(25):14827-32 (1996). Moreover, high level expression of APOBEC1 in transgenic mice and rabbit livers causes liver dysplasia and hepatocellular carcinomas and guanylate cyclase 2C appears to be relatively specific marker for the presence of metastatic colonic carcinoma cells. These observations, together with the appearance of the guanylate cyclase 2C in tumor specific clusters, indicate that this gene is a putative marker of progression of colon cancer.

EXAMPLE 2

[000104] In order to detect the presence of a tumor associated EST in actual tissue samples, biological samples were prepared and analyzed for the presence or absence of the EST sequence. In each case, where clusters are defined by a plurality of sequences, the probes utilized are derived from the longest reported sequence for the cluster. Individual subsets of EST clusters predicted to be tumor associated with the methods of the present invention were analyzed in polymerase chain reaction studies on Clontech multiple tissues cDNA (MTC) panels and on panels of genomic DNA from different animal species. Gene or gene fragments corresponding to EST clusters Hs.133107,

Hs. 154173 and Hs. 67624 according to our computational differential display studies were expressed only in tumors. Hs. 133244 was expressed in a variety of tumors and was also expressed at very low levels in normal testis and germinal B-cells. Initially, the screening method involved a non-PCR based strategy. Such screening methods include two-step label amplification

5 methodologies that are well known by persons of ordinary skill in the art. Both PCR and non-PCR based screening strategies can also detect target sequences with a high level of sensitivity.

[000105] A subset of EST clusters found by HSAlyst software was analyzed by both confirmatory PCR on Clontech Multiple Tissue cDNA Panels. PCR Amplification of the tumor associated EST Hs.133294 Fragment was analyzed in Human Tumor MTC Panel 1 and 2, Human
10 Immune System MTC Panel, Human Fetal MTC Panel, DNA from Different Animal species, and Southern hybridization of Hs.133294 fragment with genomic DNA from different animal species digested to completion with EcoR I. Hs.133294 represents an EST protein-encoding mRNA located on chromosome 1q21. It is weakly similar in homology to IQGA (human RAS GTPase-activating-like protein IQGAP1). Hs.133294 was represented in: prostate tumor, HNSCC, breast carcinoma,
15 oligodendroglioma, colon carcinoma, CML, lung carcinoma, ovarian carcinoma, uterus carcinoma, adrenal adenoma and «minor occurrences» in normal testis and germinal B-cells. One EST in the cluster was derived from normal testis, one from germinal B-cells and twenty-five from different tumors. Both testis and germinal B-cells as tissues are known to express tumor markers, e.g. cancer-testis antigen family members are expressed only in testis in a healthy organism, but testis
20 expression does not interfere with the tumor marker features of such a genes. Unlike in the case of the other examples contained herein, where primers were selected from the same exon, in this case primers belong to two different exons separated by intron 672bp in size. That is why two fragments may be considered as specific to Hs.133294: a 1084 bp fragment which corresponds to unspliced mRNA and a 412 bp fragment corresponding to spliced mRNA. PCR on human tumor MTC panel
25 produced the 1084 bp fragment on cDNAs from all eight tumors comprising the panel. The 412 bp fragment was not generated in samples from prostatic adenocarcinoma, lung carcinoma and colon adenocarcinoma propagated as xenografts in athymic nude mice. The 412 bp fragment was generated in lung carcinoma and colon adenocarcinoma which have been taken as surgical explants from metastasis and primary tumor. PCR of cDNA from testis generated the 412 bp fragment
30 detected in normal human MTC panels 1 and 2 and weak detection of the 1084 bp fragment. No

fragments were produced on human immune system MTC panel. But on human fetal MTC panel both 1084 bp and 412 bp fragments were amplified in cDNAs from all organs and/or tissues represented in the panel. One thousand eighty four base pairs fragment corresponding to unspliced mRNA was detected in all lanes in relatively greater amounts than the 412 bp fragment. The weakest signals for both fragments were detected for fetal brain and heart.

EXAMPLE 3

[000106] Utilizing similar methods as in Example 2, Hs.154173, a non-coding mRNA with tumor expression located in the intergenic spacer region within the rRNA encoding unit and is represented in lung carcinoma and testicular teratocarcinoma was analyzed for expression in the various tissue panels as in Example 2. PCR testing with Hs. 154173 specific primers on human tumor MTC panel resulted in amplification of an Hs.154173-specific fragment of 443 bp in the lanes corresponding to breast carcinoma and pancreatic adenocarcinoma. There was also a weak band in the lane that corresponded to prostatic adenocarcinoma.

[000107] In contrast, PCR analysis with the same Hs.154173-specific primers on normal human MTC panels 1 and 2; on human immune system MTC panel and human fetal MTC panel demonstrated no amplification of the corresponding fragment in any of 31 normal tissues cDNA comprising these four normal panels, indicating that this fragment is not expressed in these tissues.

EXAMPLE 4

[000108] Hs.67624 is a tumor-associated non coding mRNA located on Chromosome 3 and represented in germ cell tumors and head and neck squamous cell carcinoma. The results of PCR amplification of the tumor associated EST Hs.67624 fragment in Human Tumor MTC Panel 1 and 2, Human Immune System MTC Panel, Human Fetal MTC Panel, DNA from different animal species, and Southern hybridization of Hs.67624 fragment with genomic DNA from different animal species on genomic DNA digested to completion with EcoRI. These results confirmed that HS 67624 as a tumor associated EST expressed in ovarian carcinoma. There are three human tissues that often express tumor antigens. These are thymus, testis and embryonic tissues. PCR with Hs. 67624-specific primers on human tumor MTC panel resulted in predicted amplification of 315 bp

Hs. 67624-specific fragment in ovarian carcinoma. PCR with the same Hs.67624 primers on normal human MTC panels 1 and 2 resulted in no fragments on any of 16 normal cDNA libraries comprising these panels. PCR on human immune system MTC panel and human fetal MTC panel produced signals corresponding to 315 bp fragment only on cDNA from thymus. The signal in fetal thymus was considerably stronger than for normal thymus.

EXAMPLE 5

[000109] Hs.133107 is a tumor associated non-coding mRNA located on chromosome 12p13. The results of PCR Amplification of the EST Hs.133107 fragment in Human Tumor MTC Panel 1 and 2, Human Immune System MTC Panel, Human Fetal MTC Panel. These results confirmed that Hs. 133107 as a tumor related EST. PCR on normal Human MTC Panels 1 and 2 produced no fragments on any of cDNA from 16 normal tissues. PCR on human immune system MTC panel resulted in amplification of 344 bp fragment on cDNA from lymph node. PCR on human fetal MTC panel did not result in any fragments.

EXAMPLE 6

[000110] The results of PCR Amplification of the a nucleic acid specific for Glucose 3 phosphate dehydrogenase fragment in Human Tumor MTC Panel 1 and 2, Human Immune System MTC Panel, Human Fetal MTC Panel and DNA from different animal species was performed as in the above examples. This control demonstrated that mRNA specific for Glucose 3 phosphate dehydrogenase could be detected in a manner consistent with known expression patterns of this gene.

EXAMPLE 7

[000111] The methods of the present invention were used to detect differential expression of genes expressed in hyperosmotic stress (caused by NaCl), or dehydration in the plant *Arabidopsis thaliana*. Despite the relatively small number of ESTs and UNIGENE clusters available for this organism, 5 stress-associated clusters were detected using the methods of the present invention. Three stress-associated clusters detected in *A. thaliana* represented known plant genes involved in

stress response: GST30, Lti30 and cor15-encoding gene. The remaining clusters represented unknown genes. The applicability of the methods of the present invention to *A. thaliana* provides a prognostic model useful to determine if the relevant genes found in *A. thaliana* can be used as a hybridization templates to find orthologs in other agricultural plants and such orthologs will be useful for gene targeting etc in such important plants.

[000112] Utilizing the methods of the present invention, a database "AT Lib Registry" was constructed. This database contained descriptions of all cDNA expression libraries used to build an EST database for *A. thaliana*. Computer-based methods were used to determine mRNA sequences differentially expressed in plants under different physiological conditions including oxidative, herbicidal and other stress types. The CDD permitted an analysis of the absolute number of nucleotide sequences synthesized for transcription matrices of every type of interest in discovered samples. The CDD analysis utilized data from databases such as dbEST containing more than 110 000 EST sequences that were deduced from cDNA libraries made from *A. thaliana* cells. For every sequence in the database there was a description of source cDNA library provided. These data and the EST clustering information complete the dataset needed to describe a tissue-associated (or condition-associated) expression of transcripts of every type (or genes). The processing of large volumes of EST information was facilitated by means of a variation of the Hs.Analyst software utilized for determination of tumor-associated markers wherein the variation utilized the Hs.Analyst main module and an Arabidopsis LibRegistry, dividing the Arabidopsis libraries according to stress/non-stress categories.

[000113] The software At_Analyst was utilized to analyze EST clustering data of the model plant *Arabidopsis thaliana* and to conduct a comparative analysis of gene expression spectra in different tissues of the plant. In this example, all data sources were divided into 3 classes named "target1", "target2" and "undefined", whereas the last class pooled data were not entered in either of first two classes.

[000114] **At_Analyst software description.** In this example, the source data for the program were arranged in two plain text files designated "at.data" and "libraries". The file "at.data" contained cluster descriptions arranged according to individual clusters. All fields were listed each in a separate line for each EST. Each cluster description with a field "ID" which contained the

internal UniGene cluster index, the cluster gene "title" and gene name if there was significant known homology of a cluster to a known gene, the number of sequences of any type (mRNA, protein, cDNA) included in cluster and lines containing information about all individual sequences of the cluster. For each sequence there was provided a LID (Library ID) which data field was LID used to retrieve information about the EST source library, thereby allowing association of the EST sequence with a particular physiological state or growth condition.

[000115] The database "At Library Registry" was created. This database included all source cDNA clone library descriptions of 71 libraries prepared from different parts or tissues of *A. thaliana*. Every record consisted of the following fields: 1) library ID in dbEST database; 2) library name; 3) tissue source of mRNA used to prepare cDNA sequences and additional comments concerning library construction methods and physiological conditions of plant growth; 4) organism name (*A. thaliana* in the present example); 5) organism strain or ecotype; and 6) cloning vector used for library construction. In general, source tissues were derived from *A. thaliana* strains Columbia Col-0, Columbia C24, Columbia GH50, Columbia gl1, Landsberg erecta and Ohio State. Some of the libraries in the database were obtained from plant parts like aboveground organs, roots, flower buds, green siliques, immature siliques, inflorescence, rosettes, seedling hypocotyls and some from different specific cell types. There were also included a number of clone libraries made from cultured cell lines of *A. thaliana*.

[000116] All clone libraries in the At Library Registry were separated into four general types: 1) "untreated" indicated clone libraries made from normal plants and its parts cultivated under normal conditions; 2) "treated" – indicated libraries made from plants subjected to any kind of stressing; 3) "low-level" indicated clone libraries prepared from genomic DNA, not on mRNA; 4) "undefined" – indicated clone libraries whose origin could not be deduced with the available information. The resulting base AT Library Registry was presented by a Microsoft Excel workbook consisting of four worksheets, one for each type of clone library class as mentioned above. The total number of sequences that were derived from clone libraries included in AT Library Registry was 113 023 ESTs.

[000117] A round of CDD was conducted when we found quantitative percentages of transcription pools volumes of plants exposed to stress conditions and plants grew in normal physiological conditions. Statistical analysis of expression spectra has revealed the quantitatively reliable differences among plants exposed to salt (hyperosmotic) stresses. The results are presented in Table 3. The conditions for comparing the clusters compared EST's from stress-induced Arabidopsis to normal plants contained EST's expressed in stress-exposed plants. Genes (clusters) of interest demonstrated to be associated with Arabidopsis stress conditions were At.11290 (glutathione S-transferase), At.5388 (lti30) and At.20845 (COR15 polypeptide).

10

Table III Sequences of clusters differentially expressed under salt stress conditions.

Cluster ID	Gene presented by cluster	All sequences	Protein sequences	Target sequences	Background sequences
At.5801	Arabidopsis thaliana AT3g28220/T19D11_3 mRNA, complete cds	10	2	7	1
At.5388	<i>Arabidopsis thaliana</i> (Landsberg Erecta) lti30 mRNA	13	3	8	1
At.11290	Arabidopsis thaliana chromosome I glutathione S-transferase (GST30) mRNA, complete cds	13	3	8	2
At.12464	Arabidopsis thaliana chromosome II section 206 of 255 of the complete sequence. Sequence from clones P16M14	13	1	11	1
At.20845	<i>Arabidopsis thaliana</i> mRNA for COR15 polypeptide	32	4	24	4

[00118] The methods of the present invention are also applicable to other agricultural plants that are well represented in the UniGene database. For example, as of 20 November 2001, there were 34812 sequences in 4012 clusters for *Hordeum vulgare*, 47841 sequences in 12836 clusters for *Oryza sativa*, 31826 sequences in 2744 clusters for *Triticum aestivum* and 69231 sequences in 7171 clusters for *Zea mays*. Furthermore, the methods of the present invention may be applied to other organisms additional datasets are developed that build clusters similar to UniGene database. There are 208198 sequences available for Glycine max, 141687 sequences for Lycopersicon esculentum, 137588 sequences for Medicago truncatula, 76645 sequences for Sorghum bicolor and 55637 sequences for Solanum tuberosum. Since about 113 000 sequences were enough to obtain statistically reliable results in our investigation it is reasonable to recommend using of CDD method for searching for stress-induced genes in the above mentioned plants as done with Arabidopsis.

[000119] The investigation of *Arabidopsis thaliana* associated ESTs derived from clone libraries made from the stress-exposed and normal plants revealed three genes that encoded proteins that were overexpressed-in-stress proteins (as used herein, the term "stress-overexpressed applies to the fact that 80% or more of the sequences from their clusters are derived from plant grown in stress conditions. The available clone libraries were also adequate for investigation of salt-induced stress. Thus, seven of eight total ESTs in cluster AT.5801 were derived from library m27 made from 10-14-days old shoots treated by 160mM NaCl solution for several hours. Eight of a total of nine ESTs of cluster At.11290 are also derived from this clone library. Cluster At.20845 consists of 22 ESTs from the same clone library 27, 2 ESTs from the plant parts treated by 200 mM NaCl (library numbers 15 and 40) and 4 ESTs from the parts of normal plant. Library 27 was deliberately enriched by sequences specifically expressed in salt stressed plant whereas libraries 15 and 40 were not as can be seen quite clearly from the typical stress-induced cluster structures (as e.g., At.20845). It is clear also that the CDD methods of the present invention are more productive than an experimental approach which is not sensitive enough to distinguish between low levels of expression of salt-induced genes.

[000120] One of the revealed clusters At.11290 represented the glutathione-S-transferase gene (GST30). It is known that glutathione transferases are involved in different stress-induced pathways. For example the expression of one of these transferases is increasing the plant's resistance for the aluminum abundance. Moreover, it was shown that such plants are display a

significant increase of oxidative stress resistance which can be seen when straining the plant's roots with H(2)DCFDA (Ezalki B. et al., 2001 *Plant Physiol* 2001 Nov;127(3):918-927). It is also known that the induction of glutathione-S-transferases occurs when the plant is infected with *Peronospora parasitica* or *Pseudomonas syringae* pv. *Tomato*, when the plant is treated by some kind of herbicides and even when the leaf structure is broken (Rairdan GJ et al., 2001 *Mol Plant Microbe Interact* 2001 Oct;14(10):1235-46; Vollenweider S et al., 2000 *Plant J* 2000 Nov;24(4):467-76). The level of glutathione-S-transferase gene also increases when the plant cells are treated with auxine, salicylic acid or hydrogenic peroxide (Chen W. Singh KB 1999 *Plant Physiol* 2001 Nov;127(3):918-927). As it can be deduced from published data the glutathione-S-transferase gene is often overexpressed under different kinds of stress conditions in plants. Nevertheless as it is shown in our work, this gene is specifically expressed under salt stress conditions and may serve as marker for this kind of stress.

[000121] The other revealed cluster At.5388 represents the gene *lti30* coding dehydrin *lti30* which synthesis is induced under the low-temperature stress but not in plants treated by abscisic acid or drought or cold (Welin B.V. et al., 1994 *Plant Mol Biol* 1994 Oct;26(1):131-44). The cluster At.20845 is representing *cor15* protein which shows even more cryoprotective activity than BSA or saccharose (Lin C, Thomashow MF, 1992 *Biochem Biophys Res Commun* 1992 Mar 31;183(3):1103-8). So far as both genes were revealed in our CDD experiments with salt stress-induced genes it might be reasonable to suppose a common underlying processes of regulation of the salt- and temperature-induced plant response.

CLAIMS

What is claimed is:

1. A method for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species which comprises:
 - 5 (a) providing a database of expressed sequence tag sequences (EST's) from the species;
 - (b) placing said EST's in groups termed clusters based on homology of EST's within each cluster;
 - (c) determining for each cluster the total number of EST's within said cluster;
 - (d) ordering said clusters sequentially based on the number of EST's in each cluster;
 - 10 (e) dividing said ordered clusters into subranges based on the number of EST's per cluster;
 - (f) determining for each cluster subrange obtained from step (e) the number EST's within said cluster which are expressed in said predetermined cell type of interest;
 - (g) calculating according to a normal distribution the number of clusters in each subrange expected to contain a predetermined threshold percentage of EST's expressed in said cell type of
 - 15 interest, wherein said threshold percentage is a percentage from about 10% to about 100%;
 - (h) determining the number of clusters in each subrange observed to contain said predetermined threshold percentage of EST's expressed in said predetermined cell type; and
 - (i) identifying subranges having an observed number of clusters that meet said predetermined threshold percentage greater than the number of clusters expected to meet said
 - 20 predetermined threshold percentage for the subrange according to normal distribution;
 - wherein if the percentage of EST's expressed in said cell type of interest in a cluster identified in (i) is equal to or greater than said predetermined threshold percentage, said cluster contains a nucleic acid that is a marker for the cell type of interest.
- 25 2. The method of claim 1 wherein one or more of the steps are performed on a computer.
3. The method of claim 1 wherein the individual clusters are divided into subranges exponentially.

4. The method of claim 1 wherein the individual clusters are divided into subranges linearly.
5. The method of claim 1 wherein the predetermined threshold percentage of EST's expressed in said cell type of interest is a percentage of about 50% to 100%.
5
6. The method of claim 1 wherein the predetermined threshold percentage of EST's expressed in said cell type of interest is a percentage of about 70% to 100%.
7. The method of claim 1 wherein the predetermined threshold percentage of EST's expressed in said cell type of interest is a percentage of about 80% to 100%.
10
8. The method of claim 1 wherein the predetermined threshold percentage of EST's expressed in said cell type of interest is a percentage of about 90% to 100%.
9. The method of claim 1 wherein the predetermined threshold percentage of EST's expressed in said cell type of interest is a percentage of at least 80%.
15
10. The method of claim 1 wherein the predetermined threshold percentage of EST's expressed in said cell type of interest is a percentage of at least 90%.
20
11. The method of claim 1 wherein the predetermined threshold percentage of EST's expressed in said cell type of interest is a percentage of at least 95%.
12. The method of claim 1 wherein the predetermined threshold percentage of EST's expressed in said cell type of interest is a percentage of 100%.
25
13. A method as in claim 1 wherein the cell type of interest is an abnormal cell.

14. The method of claim 1 or claim 13 wherein step (i) comprises identifying subranges having an observed number of clusters meeting said predetermined threshold percentage at least five times greater than the number expected for the subrange according to normal distribution.
- 5
15. The method of claim 1 or claim 13 wherein step (i) comprises identifying subranges having an observed number of clusters meeting said predetermined threshold percentage at least one standard deviation greater than the number expected for the subrange according to normal distribution.
- 10
16. The method of claim 1 or claim 13 wherein the species is human.
17. The method of claim 16 wherein the individual clusters are divided into subranges exponentially.
- 15
18. The method of claim 16 wherein the individual clusters are divided into subranges exponentially.
19. The method of claim 16 wherein the predetermined threshold percentage of EST's expressed in a tumor cell is at least 90%.
- 20
20. The method of claim 16 wherein the predetermined threshold percentage of EST's expressed in a tumor cell is 95%.
21. The method of claim 16 wherein the predetermined threshold percentage of EST's expressed in
- 25
- a tumor cell is 100%.
22. A method for determining the progression of colon cancer in a human which comprises determining the level of expression of guanylate cyclase 2C in a cell, wherein if the level of

guanylate cyclase 2C expression is greater than the level of expression of guanylate cyclase 2C in normal cells, said cell is a tumor cell.

23. The method of claim 22 wherein the level of the guanylate cyclase 2C is detected by
5 determining the level of mRNA expression for the guanylate cyclase 2C gene.

24. An isolated antibody which specifically binds to a tumor-associated antigen encoded by a nucleic acid selected from the group consisting of SEQ ID NO:'s 9, 11, 13, 15, 17, 19, 23, 25, 27, 29, 33, 35, 37, 39, 41, 45, 47, 55, 57, 59, 61, 63, 65, 67, 69, 73, 75, 77, 79, 81, 83, 89, 91, 93, 95,
10 97, 99, 101, 103, 107, 109, 111, 113, 115, 117, 119, 121, 123, 127, 129, 131, 133, 135, 137, 138, 140, 142, 144, 146, 148, 150, 153, 155, 157, 158, 160, 162, 164, 166, 168, 172, 174, 176, 178, 180, 182, 184, 186, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300,
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25. An isolated antibody as in claim 24 wherein the nucleic acid is encoded by a sequence selected
20 from the group consisting of SEQ ID NO:'s 73, 184, 186 and 242.

26. An isolated antibody as in claim 24 which further comprises a toxin.

27. A method for detecting a tumor cell which comprises detecting the expression in said cell of a
25 tumor-associated marker, wherein said marker is a nucleic acid selected from the group of nucleic acids in claim 24.

28. A method as in claim 27 wherein the nucleic acid marker is selected from the group consisting of SEQ ID NO:s 73, 184, 186 and 242.

29. A method for detecting a tumor cell which comprises detecting the expression in said cell of a
5 tumor-associated marker, wherein said marker is a polypeptide selected from the group consisting
of SEQ ID NO:s 10, 12, 14, 16, 20, 24, 46, 28, 30, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58,
60, 62, 64, 66, 68, 70, 71, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106,
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15 397, 399, 401, 403, 405, 407, 409, 411, 413 and 415.

30. A method as in claim 29 wherein the polypeptide marker is selected from the group consisting of sequence selected from the group consisting of SEQ ID NO:s 74, 185, 187, 188 and 243.

20 31. A method for regulating the growth of a tumor cell which comprises altering the level of
expression of a tumor-associated marker, wherein said marker is a nucleic acid selected from the
group of nucleic acids of claim 24.

32. A method as in claim 31 wherein the nucleic acid marker is selected from the group consisting
25 of sequences selected from the group consisting of SEQ ID NO:s 73, 184, 186 and 242.

33. A method as in claim 31 wherein the level of expression of the tumor-associated marker is
regulated with an siRNA.

34. A method for regulating the growth of a tumor cell which comprises altering the level of expression of a tumor marker, wherein said marker is a polypeptide selected from the group of polypeptides of claim 29.

5

35. A method as in claim 34 wherein the polypeptide is selected from the group consisting of sequence selected from the group consisting of SEQ ID NO:'s 74, 185, 187, 188 and 243.

10

36. A method for preventing the growth of a tumor cell which comprises treating the cell with an antibody specific for a tumor-associated antigen wherein the antigen comprises a polypeptide as in claim 29.

37. A method as in claim 34 wherein the tumor marker is a polypeptide selected from the polypeptides of SEQ ID NO:'s 74, 185, 187, 188 and 242.

15

38. A method as in claims 36 or 37 wherein said antibody further comprises a toxin.

39. An isolated polypeptide for use as an immunogen, wherein said polypeptide is selected from the group of polypeptides of claim 29.

20

39. The isolated peptide of claim 37 or 38 which comprises an epitope reactive with a Cytotoxic T-cell.

25

40. A method for determining whether a nucleic acid is a marker for a stress-induced phenotype in a species which comprises:

- (a) providing a database of expressed sequence tag sequences (EST's) from the species;
- (b) placing said EST's in groups termed clusters based on homology of EST's within each cluster;

- (c) determining for each cluster the total number of EST's within said cluster;
- (d) ordering said clusters sequentially based on the number of EST's in each cluster;
- (e) dividing said ordered clusters into subranges based on the number of EST's per cluster;
- (f) determining for each cluster subrange obtained from step (e) the number EST's within
5 said cluster which are expressed in a cell under said stress conditions;
- (g) calculating according to a normal distribution the number of clusters in each subrange expected to contain a predetermined threshold percentage of EST's expressed in a cell under said stress conditions, wherein said threshold percentage is a percentage from about 10% to about 80%;
- (h) determining the number of clusters in each subrange observed to contain said
10 predetermined threshold percentage of EST's expressed in said cell; and
- (i) identifying subranges having an observed number of clusters that meet said predetermined threshold percentage greater than the number of clusters expected to meet said predetermined threshold percentage for the subrange according to normal distribution;
wherein if the percentage of EST's expressed in said cell type of interest in a cluster
15 identified in (i) is equal to or greater than said predetermined threshold percentage, said cluster contains a nucleic acid marker that is a marker for the stress-induced phenotype.

- 41. The method of claim 40 wherein one or more of the steps are performed on a computer.
- 20 42. The method of claim 40 wherein the individual clusters are divided into subranges exponentially.
- 43. The method of claim 40 wherein the individual clusters are divided into subranges linearly.
- 25 44. The method of claim 40 wherein the predetermined threshold percentage of EST's expressed in said cell type of interest is a percentage of about 80%.
- 45. The method of claim 40 wherein the species is *Arabidopsis*.

46. The method of claims 40 or 45 wherein the stress-induced phenotype is selected from the group consisting of hyperosmotic stress and high salt conditions.

5 47. A method for determining whether a nucleic acid is a marker for a tumor cell from a human which comprises:

- (a) providing a database of expressed sequence tag sequences (EST's) from human tumor cells and human normal cells;
 - (b) placing said EST's in groups termed clusters based on homology of EST's within each
10 cluster;
 - (c) determining for each cluster the total number of EST's within said cluster;
 - (d) ordering said clusters sequentially based on the number of EST's in each cluster;
 - (e) dividing said ordered clusters into subranges based on the number of EST's per cluster;
 - (f) determining for each cluster subrange obtained from step (e) the number EST's within
15 said cluster which are expressed in a tumor cell;
 - (g) calculating according to a normal distribution the number of clusters in each subrange expected to contain a predetermined threshold percentage of EST's expressed in said human tumor cells, wherein said threshold percentage is a percentage from about 10% to about 100%;
 - (h) determining the number of clusters in each subrange observed to contain said
20 predetermined threshold percentage of EST's expressed in a tumor cell; and
 - (i) identifying subranges having an observed number of clusters that meet said predetermined threshold percentage greater than the number of clusters expected to meet said predetermined threshold percentage for the subrange according to normal distribution;
- wherein if the percentage of EST's expressed in said cell type of interest in a cluster
25 identified in (i) is equal to or greater than said predetermined threshold percentage, said cluster contains a nucleic acid that is a marker for a tumor cell.

48. The method of claim 47 wherein one or more of the steps are performed on a computer.

49. The method of claim 47 wherein the individual clusters are divided into subranges exponentially.

50. The method of claim 47 wherein the individual clusters are divided into subranges linearly.

5

51. The method of claim 47 wherein the predetermined threshold percentage of EST's expressed in said cell type of interest is a percentage of about 80% to 100%.

52. The method of claim 47 wherein the predetermined threshold percentage of EST's expressed in
10 said cell type of interest is a percentage of at least 90%.

53. The method of claim 47 wherein the predetermined threshold percentage of EST's expressed in said cell type of interest is a percentage of 100%.

15 54. The method of claim 47 wherein step (i) comprises identifying subranges having an observed number of clusters meeting said predetermined threshold percentage at least five times greater than the number expected for the subrange according to normal distribution.

20 55. The method of claim 47 wherein step h consists of (i) identifying subranges having an observed number of clusters meeting said predetermined threshold percentage at least one standard deviation greater than the number expected for the subrange according to normal distribution.

SEQUENCE LISTING

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<210> 12
 <211> 328
 <212> PRT
 <213> Homo sapiens

<400> 12

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Ile Ala Ala Ser Ser Thr Tyr His Gln His Gln Gln Pro Pro Ser Gly
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Gly Gly Ala Gly Pro Gly Gly Asn Ser Ser Ser Ser Ser Ser Leu His
 35 40 45

Lys Pro Gln Glu Ser Pro Thr Leu Pro Val Ser Thr Ala Thr Asp Ser
 50 55 60

Ser Tyr Tyr Thr Asn Gln Gln His Pro Ala Gly Gly Gly Gly Gly Gly
 65 70 75 80

Gly Ser Pro Tyr Ala His Met Gly Ser Tyr Gln Tyr Gln Ala Ser Gly
 85 90 95

Leu Asn Asn Val Pro Tyr Ser Ala Lys Ser Ser Tyr Asp Leu Gly Tyr
 100 105 110

Thr Ala Ala Tyr Thr Ser Tyr Ala Pro Tyr Gly Thr Ser Ser Ser Pro
 115 120 125

Ala Asn Asn Glu Pro Glu Lys Glu Asp Leu Glu Pro Glu Ile Arg Ile
 130 135 140

Val Asn Gly Lys Pro Lys Lys Val Arg Lys Pro Arg Thr Ile Tyr Ser
 145 150 155 160

Ser Phe Gln Leu Ala Ala Leu Gln Arg Arg Phe Gln Lys Thr Gln Tyr
 165 170 175

Leu Ala Leu Pro Glu Arg Ala Glu Leu Ala Ala Ser Leu Gly Leu Thr
 180 185 190

Gln Thr Gln Val Lys Ile Trp Phe Gln Asn Arg Arg Ser Lys Phe Lys
 195 200 205

Lys Met Trp Lys Ser Gly Glu Ile Pro Ser Glu Gln His Pro Gly Ala
 210 215 220

Ser Ala Ser Pro Pro Cys Ala Ser Pro Pro Val Ser Ala Pro Ala Ser
 225 230 235 240

Trp Asp Phe Gly Val Pro Gln Arg Met Ala Gly Gly Gly Gly Pro Gly
 245 250 255

Ser Gly Gly Ser Gly Ala Gly Ser Ser Gly Ser Ser Pro Ser Ser Ala
 260 265 270

Ala Ser Ala Phe Leu Gly Asn Tyr Pro Trp Tyr His Gln Thr Ser Gly
 275 280 285

Ser Ala Ser His Leu Gln Ala Thr Ala Pro Leu Leu His Pro Thr Gln
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Thr Pro Gln Pro His His His His His His His Gly Gly Gly Gly Ala
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Pro Val Ser Ala Gly Thr Ile Phe
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<210> 13
 <211> 879
 <212> DNA
 <213> Homo sapiens

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 gatctacgta gctcggcttt tttggcacat ggatcaacaa aatcggcaag gtctcaggga 420
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 gaggaatttt gtcaactacc cacctgggga tgaagctcac tggccacaat acccacctct 540
 gtggatgatg ttgtacgcac tggagctgca ctgcataatt ctaagtcttc caccctgttt 600
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<210> 14
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 14

Met Thr Ser Glu Lys Gly Pro Ser Thr Gly Asp Pro Thr Leu Arg Arg
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Arg Ile Glu Pro Trp Glu Phe Asp Val Phe Tyr Asp Pro Arg Glu Leu
 20 25 30

Arg Lys Glu Ala Cys Leu Leu Tyr Glu Ile Lys Trp Gly Met Ser Arg
 35 40 45

Lys Ile Trp Arg Ser Ser Gly Lys Asn Thr Thr Asn His Val Glu Val
50 55 60

Asn Phe Ile Lys Lys Phe Thr Ser Glu Arg Asp Phe His Pro Ser Met
65 70 75 80

Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Trp Glu Cys
85 90 95

Ser Gln Ala Ile Arg Glu Phe Leu Ser Arg His Pro Gly Val Thr Leu
100 105 110

Val Ile Tyr Val Ala Arg Leu Phe Trp His Met Asp Gln Gln Asn Arg
115 120 125

Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln Ile Met
130 135 140

Arg Ala Ser Glu Tyr Tyr His Cys Trp Arg Asn Phe Val Asn Tyr Pro
145 150 155 160

Pro Gly Asp Glu Ala His Trp Pro Gln Tyr Pro Pro Leu Trp Met Met
165 170 175

Leu Tyr Ala Leu Glu Leu His Cys Ile Ile Leu Ser Leu Pro Pro Cys
180 185 190

Leu Lys Ile Ser Arg Arg Trp Gln Asn His Leu Thr Phe Phe Arg Leu
195 200 205

His Leu Gln Asn Cys His Tyr Gln Thr Ile Pro Pro His Ile Leu Leu
210 215 220

Ala Thr Gly Leu Ile His Pro Ser Val Ala Trp Arg
225 230 235

<210> 15

<211> 1718

<212> DNA

<213> Homo sapiens

<400> 15

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<210> 16
 <211> 453
 <212> PRT
 <213> Homo sapiens

<400> 16

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Ser Gly Arg Thr Arg Pro Leu Gln Phe Arg Ile Gln Gln Leu Glu Ala
 20 25 30

Leu Gln Arg Leu Ile Gln Glu Gln Glu Gln Glu Leu Val Gly Ala Leu
 35 40 45

Ala Ala Asp Leu His Lys Asn Glu Trp Asn Ala Tyr Tyr Glu Glu Val
 50 55 60

Val Tyr Val Leu Glu Glu Ile Glu Tyr Met Ile Gln Lys Leu Pro Glu
 65 70 75 80

Trp Ala Ala Asp Glu Pro Val Glu Lys Thr Pro Gln Thr Gln Gln Asp
 85 90 95

Glu Leu Tyr Ile His Ser Glu Pro Leu Gly Val Val Leu Val Ile Gly
 100 105 110

Thr Trp Asn Tyr Pro Phe Asn Leu Thr Ile Gln Pro Met Val Gly Ala
 115 120 125

Ile Ala Ala Gly Asn Ala Val Val Leu Lys Pro Ser Glu Leu Ser Glu
 130 135 140

Asn Met Ala Ser Leu Leu Ala Thr Ile Ile Pro Gln Tyr Leu Asp Lys
 145 150 155 160

Asp Leu Tyr Pro Val Ile Asn Gly Gly Val Pro Glu Thr Thr Glu Leu
 165 170 175

Leu Lys Glu Arg Phe Asp His Ile Leu Tyr Thr Gly Ser Thr Gly Val
 180 185 190

Gly Lys Ile Ile Met Thr Ala Ala Ala Lys His Leu Thr Pro Val Thr

195	200	205																	
Leu	Glu	Leu	Gly	Gly	Lys	Ser	Pro	Cys	Tyr	Val	Asp	Lys	Asn	Cys	Asp				
210						215					220								
Leu	Asp	Val	Ala	Cys	Arg	Arg	Ile	Ala	Trp	Gly	Lys	Phe	Met	Asn	Ser				
225					230					235					240				
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Arg	His	Phe	Gln	Arg	Val	Met	Gly	Leu	Ile	Glu	Gly	Gln	Lys	Val	Ala				
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Tyr	Gly	Gly	Thr	Gly	Asp	Ala	Ala	Thr	Arg	Tyr	Ile	Ala	Pro	Thr	Ile				
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Gly	Pro	Val	Leu	Pro	Ile	Val	Cys	Val	Arg	Ser	Leu	Glu	Glu	Ala	Ile				
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Gln	Phe	Ile	Asn	Gln	Arg	Glu	Lys	Pro	Leu	Ala	Leu	Tyr	Met	Phe	Ser				
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Gly	Val	Ala	Ala	Asn	Asp	Val	Ile	Val	His	Ile	Thr	Leu	His	Ser	Leu				
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Pro	Phe	Gly	Gly	Val	Gly	Asn	Ser	Gly	Met	Gly	Ser	Tyr	His	Gly	Lys				
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Lys	Ser	Phe	Glu	Thr	Phe	Ser	His	Arg	Arg	Ser	Cys	Leu	Val	Arg	Pro				

420

425

430

Leu Met Asn Asp Glu Gly Leu Lys Val Arg Tyr Pro Pro Ser Pro Ala
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Lys Met Thr Gln His
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<210> 17

<211> 3745

<212> DNA

<213> Homo sapiens

<400> 17

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<210> 18
<211> 1073
<212> PRT
<213> Homo sapiens

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<400> 18
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Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe Gln
1          5          10          15

```

```

Pro Gly Trp Leu Ser Phe Ser Ser Gln Val Ser Gln Asn Cys His Asn
20          25          30

```

```

Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser Ala Phe Ala
35          40          45

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```

Glu Pro Leu Lys Asn Leu Glu Asp Ala Val Asn Glu Gly Leu Glu Ile
50          55          60

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Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala
65          70          75          80

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Thr Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg
 85 90 95

Ser Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala
 100 105 110

Gln Arg Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser Thr
 115 120 125

Phe Gln Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala
 130 135 140

Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu
 145 150 155 160

Met Ser Pro Ala Arg Lys Leu Met Tyr Phe Leu Val Asn Phe Trp Lys
 165 170 175

Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val
 180 185 190

Tyr Lys Asn Gly Thr Glu Thr Glu Asp Cys Phe Trp Tyr Leu Asn Ala
 195 200 205

Leu Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu Gly Phe Lys Val
 210 215 220

Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile Leu Met Asp His Asn
 225 230 235 240

Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly Pro Glu Phe Leu Tyr
 245 250 255

Lys Leu Lys Gly Asp Arg Ala Val Ala Glu Asp Ile Val Ile Ile Leu
 260 265 270

Val Asp Leu Phe Asn Asp Gln Tyr Leu Glu Asp Asn Val Thr Ala Pro
 275 280 285

Asp Tyr Met Lys Asn Val Leu Val Leu Thr Leu Ser Pro Gly Asn Ser
 290 295 300

Leu Leu Asn Ser Ser Phe Ser Arg Asn Leu Ser Pro Thr Lys Arg Asp
305 310 315 320

Phe Ala Leu Ala Tyr Leu Asn Gly Ile Leu Leu Phe Gly His Met Leu
325 330 335

Lys Ile Phe Leu Glu Asn Gly Glu Asn Ile Thr Thr Pro Lys Phe Ala
340 345 350

His Ala Phe Arg Asn Leu Thr Phe Glu Gly Tyr Asp Gly Pro Val Thr
355 360 365

Leu Asp Asp Trp Gly Asp Val Asp Ser Thr Met Val Leu Leu Tyr Thr
370 375 380

Ser Val Asp Thr Lys Lys Tyr Lys Val Leu Leu Thr Tyr Asp Thr His
385 390 395 400

Val Asn Lys Thr Tyr Pro Val Asp Met Ser Pro Thr Phe Thr Trp Lys
405 410 415

Asn Ser Lys Leu Pro Asn Asp Ile Thr Gly Arg Gly Pro Gln Ile Leu
420 425 430

Met Ile Ala Val Phe Thr Leu Thr Gly Ala Val Val Leu Leu Leu Leu
435 440 445

Val Ala Leu Leu Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg
450 455 460

Gln Lys Lys Trp Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu
465 470 475 480

Thr Asn Glu Thr Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg
485 490 495

Arg Asp Thr Ile Gln Arg Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg
500 505 510

Val Ile Leu Lys Asp Leu Lys His Asn Asp Gly Asn Phe Thr Glu Lys
515 520 525

Gln Lys Ile Glu Leu Asn Lys Leu Leu Gln Ile Asp Tyr Tyr Asn Leu
 530 535 540

Thr Lys Phe Tyr Gly Thr Val Lys Leu Asp Thr Met Ile Phe Gly Val
 545 550 555 560

Ile Glu Tyr Cys Glu Arg Gly Ser Leu Arg Glu Val Leu Asn Asp Thr
 565 570 575

Ile Ser Tyr Pro Asp Gly Thr Phe Met Asp Trp Glu Phe Lys Ile Ser
 580 585 590

Val Leu Tyr Asp Ile Ala Lys Gly Met Ser Tyr Leu His Ser Ser Lys
 595 600 605

Thr Glu Val His Gly Arg Leu Lys Ser Thr Asn Cys Val Val Asp Ser
 610 615 620

Arg Met Val Val Lys Ile Thr Asp Phe Gly Cys Asn Ser Ile Leu Pro
 625 630 635 640

Pro Lys Lys Asp Leu Trp Thr Ala Pro Glu His Leu Arg Gln Ala Asn
 645 650 655

Ile Ser Gln Lys Gly Asp Val Tyr Ser Tyr Gly Ile Ile Ala Gln Glu
 660 665 670

Ile Ile Leu Arg Lys Glu Thr Phe Tyr Thr Leu Ser Cys Arg Asp Arg
 675 680 685

Asn Glu Lys Ile Phe Arg Val Glu Asn Ser Asn Gly Met Lys Pro Phe
 690 695 700

Arg Pro Asp Leu Phe Leu Glu Thr Ala Glu Glu Lys Glu Leu Glu Val
 705 710 715 720

Tyr Leu Leu Val Lys Asn Cys Trp Glu Glu Asp Pro Glu Lys Arg Pro
 725 730 735

Asp Phe Lys Lys Ile Glu Thr Thr Leu Ala Lys Ile Phe Gly Leu Phe
 740 745 750

His Asp Gln Lys Asn Glu Ser Tyr Met Asp Thr Leu Ile Arg Arg Leu
 755 760 765

Gln Leu Tyr Ser Arg Asn Leu Glu His Leu Val Glu Glu Arg Thr Gln
 770 775 780

Leu Tyr Lys Ala Glu Arg Asp Arg Ala Asp Arg Leu Asn Phe Met Leu
 785 790 795 800

Leu Pro Arg Leu Val Val Lys Ser Leu Lys Glu Lys Gly Phe Val Glu
 805 810 815

Pro Glu Leu Tyr Glu Glu Val Thr Ile Tyr Phe Ser Asp Ile Val Gly
 820 825 830

Phe Thr Thr Ile Cys Lys Tyr Ser Thr Pro Met Glu Val Val Asp Met
 835 840 845

Leu Asn Asp Ile Tyr Lys Ser Phe Asp His Ile Val Asp His His Asp
 850 855 860

Val Tyr Lys Val Glu Thr Ile Gly Asp Ala Tyr Met Val Ala Ser Gly
 865 870 875 880

Leu Pro Lys Arg Asn Gly Asn Arg His Ala Ile Asp Ile Ala Lys Met
 885 890 895

Ala Leu Glu Ile Leu Ser Phe Met Gly Thr Phe Glu Leu Glu His Leu
 900 905 910

Pro Gly Leu Pro Ile Trp Ile Arg Ile Gly Val His Ser Gly Pro Cys
 915 920 925

Ala Ala Gly Val Val Gly Ile Lys Met Pro Arg Tyr Cys Leu Phe Gly
 930 935 940

Asp Thr Val Asn Thr Ala Ser Arg Met Glu Ser Thr Gly Leu Pro Leu
 945 950 955 960

Arg Ile His Val Ser Gly Ser Thr Ile Ala Ile Leu Lys Arg Thr Glu
 965 970 975

Cys Gln Phe Leu Tyr Glu Val Arg Gly Glu Thr Tyr Leu Lys Gly Arg
 980 985 990

Gly Asn Glu Thr Thr Tyr Trp Leu Thr Gly Met Lys Asp Gln Lys Phe
 995 1000 1005

Asn Leu Pro Thr Pro Pro Thr Val Glu Asn Gln Gln Arg Leu Gln
 1010 1015 1020

Ala Glu Phe Ser Asp Met Ile Ala Asn Ser Leu Gln Lys Arg Gln
 1025 1030 1035

Ala Ala Gly Ile Arg Ser Gln Lys Pro Arg Arg Val Ala Ser Tyr
 1040 1045 1050

Lys Lys Gly Thr Leu Glu Tyr Leu Gln Leu Asn Thr Thr Asp Lys
 1055 1060 1065

Glu Ser Thr Tyr Phe
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<210> 19

<211> 1274

<212> DNA

<213> Homo sapiens

<400> 19

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gggttatgag ctatcaaatg caattacatt aagacagatt atactgggca aattgagcca      180
tttagaaggt gagaatcaaa gaaacggctc tgatcctctt ttcccccttc tctctccctc      240
tccctctctc tctaaattgc agttcgtagt tccttccaat tcggaggcac aaaagtaggt      300
gagactgctt ttgtatctgc gaagtgcctc actcctgaat gtaattctag ctgagtgcga      360
tctagggttaa gagccggaca agcgggtaat tagagccgc tagctgcccg aggaccggcc      420
gccccgccaa agcgcgcccc gagtcggcgc ccttctcccg gccgagccta gctgcggtg      480
gacacggagc gcccgagatg atggtgctgg acaaggagga cggcgtgccg atgctctccg      540
tccagcccaa agggaagcag aagggtgtg cgggctgtaa ccgcaagatc aaggaccgct      600
atctgctgaa ggcattggac aagtactggc acgaagactg cctcaagtgt gcgtgctgtg      660

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actgccgcct gggcgagggtg ggctccaccc tctacaccaa ggccaacctc atcctgtgcc      720
gacgcgacta cctgaggctc tttggcacca caggaactg tgctgcttgc agcaagctga      780
tcccagcctt cgagatggtg atgcgggccc gggacaacgt gtatcaacctc gactgcttcg      840
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attagaactt ctccgtctc gatgggagg atggcccttc ctctccacc accgccgctc      1140
tgtgtgtgac ccctcctggg gccaggccg gcctgtacag totgtttct gtatataaat      1200
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<210> 20
 <211> 156
 <212> PRT
 <213> Homo sapiens

<400> 20

Met Met Val Leu Asp Lys Glu Asp Gly Val Pro Met Leu Ser Val Gln
 1 5 10 15

Pro Lys Gly Lys Gln Lys Gly Cys Ala Gly Cys Asn Arg Lys Ile Lys
 20 25 30

Asp Arg Tyr Leu Leu Lys Ala Leu Asp Lys Tyr Trp His Glu Asp Cys
 35 40 45

Leu Lys Cys Ala Cys Cys Asp Cys Arg Leu Gly Glu Val Gly Ser Thr
 50 55 60

Leu Tyr Thr Lys Ala Asn Leu Ile Leu Cys Arg Arg Asp Tyr Leu Arg
 65 70 75 80

Leu Phe Gly Thr Thr Gly Asn Cys Ala Ala Cys Ser Lys Leu Ile Pro
 85 90 95

Ala Phe Glu Met Val Met Arg Ala Arg Asp Asn Val Tyr His Leu Asp
 100 105 110

Cys Phe Ala Cys Gln Leu Cys Asn Gln Arg Phe Cys Val Gly Asp Lys
 115 120 125

Phe Phe Leu Lys Asn Asn Met Ile Leu Cys Gln Met Asp Tyr Glu Glu
 130 135 140

Gly Gln Leu Asn Gly Thr Phe Glu Ser Gln Val Gln
 145 150 155

<210> 21

<211> 2490

<212> DNA

<213> Homo sapiens

<400> 21

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agccacgggct ggagagaccg agaccggcg caagagagcg cagccttagt aggagaggaa      180
cgcgagacgc ggagagacgc gttcagcaact gacttttctg gctgcttctg cttttttttt      240
tcttagaaac aagaaggcgc cagcggcagc ctcacacgcg agcgccacgc gaggctcccg      300
aagccaaccc gcgaaggag gaggggaggg aggaggaggc ggcgtgcagg gaggagaaaa      360
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ttccgcgact ccttggccgc cgctgcgcat ggaaagctct gccaaagatgg agagcggcgg      600
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caagaagatg agtaaggtag agacactgcg ctcggcgggc gagtacatcc gcgcgctgca     1080
gcagctgctg gacgagcatg acgcggtgag cgccgccttc caggcaggcg tcctgtcgcc     1140

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<210> 22
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 22

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Met Glu Ser Ser Ala Lys Met Glu Ser Gly Gly Ala Gly Gln Gln Pro
1           5           10           15

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Gln Pro Gln Pro Gln Gln Pro Phe Leu Pro Pro Ala Ala Cys Phe Phe
 20 25 30
 Ala Thr Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Gln
 35 40 45
 Ser Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Pro
 50 55 60
 Gln Leu Arg Pro Ala Ala Asp Gly Gln Pro Ser Gly Gly Gly His Lys
 65 70 75 80
 Ser Ala Pro Lys Gln Val Lys Arg Gln Arg Ser Ser Ser Pro Glu Leu
 85 90 95
 Met Arg Cys Lys Arg Arg Leu Asn Phe Ser Gly Phe Gly Tyr Ser Leu
 100 105 110
 Pro Gln Gln Gln Pro Ala Ala Val Ala Arg Arg Asn Glu Arg Glu Arg
 115 120 125
 Asn Arg Val Lys Leu Val Asn Leu Gly Phe Ala Thr Leu Arg Glu His
 130 135 140
 Val Pro Asn Gly Ala Ala Asn Lys Lys Met Ser Lys Val Glu Thr Leu
 145 150 155 160
 Arg Ser Ala Val Glu Tyr Ile Arg Ala Leu Gln Gln Leu Leu Asp Glu
 165 170 175
 His Asp Ala Val Ser Ala Ala Phe Gln Ala Gly Val Leu Ser Pro Thr
 180 185 190
 Ile Ser Pro Asn Tyr Ser Asn Asp Leu Asn Ser Met Ala Gly Ser Pro
 195 200 205
 Val Ser Ser Tyr Ser Ser Asp Glu Gly Ser Tyr Asp Pro Leu Ser Pro
 210 215 220
 Glu Glu Gln Glu Leu Leu Asp Phe Thr Asn Trp Phe
 225 230 235

<210> 23
 <211> 2445
 <212> DNA
 <213> Homo sapiens

<400> 23
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<210> 24
<211> 653
<212> PRT
<213> Homo sapiens

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<400> 24

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Met Glu Val Ala Met Val Ser Ala Glu Ser Ser Gly Cys Asn Ser His
1          5          10          15

```

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Met Pro Tyr Gly Tyr Ala Ala Gln Ala Arg Ala Arg Glu Arg Glu Arg
20          25          30

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```

Leu Ala His Ser Arg Ala Ala Ala Ala Ala Val Ala Ala Ala Thr
35          40          45

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Ala Ala Val Glu Gly Ser Gly Gly Ser Gly Gly Gly Ser His His His
50          55          60

```

His Gln Ser Arg Gly Ala Cys Thr Ser His Asp Pro Gln Ser Ser Arg
 65 70 75 80
 Gly Ser Arg Arg Arg Arg Arg Gln Arg Ser Glu Lys Lys Lys Ala His
 85 90 95
 Tyr Arg Gln Ser Ser Phe Pro His Cys Ser Asp Leu Met Pro Ser Gly
 100 105 110
 Ser Glu Glu Lys Ile Leu Arg Glu Leu Ser Glu Glu Glu Glu Asp Glu
 115 120 125
 Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Arg Phe Tyr Tyr Ser Glu
 130 135 140
 Asp Asp His Gly Asp Glu Cys Ser Tyr Thr Asp Leu Leu Pro Gln Asp
 145 150 155 160
 Glu Gly Gly Gly Gly Tyr Ser Ser Val Arg Tyr Ser Asp Cys Cys Glu
 165 170 175
 Arg Val Val Ile Asn Val Ser Gly Leu Arg Phe Glu Thr Gln Met Lys
 180 185 190
 Thr Leu Ala Gln Phe Pro Glu Thr Leu Leu Gly Asp Pro Glu Lys Arg
 195 200 205
 Thr Gln Tyr Phe Asp Pro Leu Arg Asn Glu Tyr Phe Phe Asp Arg Asn
 210 215 220
 Arg Pro Ser Phe Asp Ala Ile Leu Tyr Tyr Tyr Gln Ser Gly Gly Arg
 225 230 235 240
 Leu Lys Arg Pro Val Asn Val Pro Phe Asp Ile Phe Thr Glu Glu Val
 245 250 255
 Lys Phe Tyr Gln Leu Gly Glu Glu Ala Leu Leu Lys Phe Arg Glu Asp
 260 265 270
 Glu Gly Phe Val Arg Glu Glu Glu Asp Arg Ala Leu Pro Glu Asn Glu
 275 280 285

Phe Lys Lys Gln Ile Trp Leu Leu Phe Glu Tyr Pro Glu Ser Ser Ser
 290 295 300

Pro Ala Arg Gly Ile Ala Ile Val Ser Val Leu Val Ile Leu Ile Ser
 305 310 315 320

Ile Val Ile Phe Cys Leu Glu Thr Leu Pro Glu Phe Arg Asp Asp Arg
 325 330 335

Asp Leu Val Met Ala Leu Ser Ala Gly Gly His Gly Gly Leu Leu Asn
 340 345 350

Asp Thr Ser Ala Pro His Leu Glu Asn Ser Gly His Thr Ile Phe Asn
 355 360 365

Asp Pro Phe Phe Ile Val Glu Thr Val Cys Ile Val Trp Phe Ser Phe
 370 375 380

Glu Phe Val Val Arg Cys Phe Ala Cys Pro Ser Gln Ala Leu Phe Phe
 385 390 395 400

Lys Asn Ile Met Asn Ile Ile Asp Ile Val Ser Ile Leu Pro Tyr Phe
 405 410 415

Ile Thr Leu Gly Thr Asp Leu Ala Gln Gln Gln Gly Gly Gly Asn Gly
 420 425 430

Gln Gln Gln Gln Ala Met Ser Phe Ala Ile Leu Arg Ile Ile Arg Leu
 435 440 445

Val Arg Val Phe Arg Ile Phe Lys Leu Ser Arg His Ser Lys Gly Leu
 450 455 460

Gln Ile Leu Gly His Thr Leu Arg Ala Ser Met Arg Glu Leu Gly Leu
 465 470 475 480

Leu Ile Phe Phe Leu Phe Ile Gly Val Ile Leu Phe Ser Ser Ala Val
 485 490 495

Tyr Phe Ala Glu Ala Asp Glu Pro Thr Thr His Phe Gln Ser Ile Pro
 500 505 510

Asp Ala Phe Trp Trp Ala Val Val Thr Met Thr Thr Val Gly Tyr Gly
515 520 525

Asp Met Lys Pro Ile Thr Val Gly Gly Lys Ile Val Gly Ser Leu Cys
530 535 540

Ala Ile Ala Gly Val Leu Thr Ile Ala Leu Pro Val Pro Val Ile Val
545 550 555 560

Ser Asn Phe Asn Tyr Phe Tyr His Arg Glu Thr Glu Asn Glu Glu Gln
565 570 575

Thr Gln Leu Thr Gln Asn Ala Val Ser Cys Pro Tyr Leu Pro Ser Asn
580 585 590

Leu Leu Lys Lys Phe Arg Ser Ser Thr Ser Ser Ser Leu Gly Asp Lys
595 600 605

Ser Glu Tyr Leu Glu Met Glu Glu Gly Val Lys Glu Ser Leu Cys Ala
610 615 620

Lys Glu Glu Lys Cys Gln Gly Lys Gly Asp Asp Ser Glu Thr Asp Lys
625 630 635 640

Asn Asn Cys Ser Asn Ala Lys Ala Val Glu Thr Asp Val
645 650

<210> 25
<211> 3336
<212> DNA
<213> Homo sapiens

<400> 25
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aatttgccaa accctgcaga gaaggagaag ataactcaaa aagaaacca attgccaaaga 300
ttacttcaga ttaccaagca acccagaaaa tcacctaccg aatctctgga gtgggaatcg 360
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atcctccagt attttcacaa caaattttca tgggtgaaat tgaagaaaat agtgcctcaa	600
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<210> 26
<211> 999
<212> PRT
<213> Homo sapiens

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<400> 26

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Met Met Gly Leu Phe Pro Arg Thr Thr Gly Ala Leu Ala Ile Phe Val
1          5          10          15

```

```

Val Val Ile Leu Val His Gly Glu Leu Arg Ile Glu Thr Lys Gly Gln
20          25          30

```

Tyr Asp Glu Glu Glu Met Thr Met Gln Gln Ala Lys Arg Arg Gln Lys
 35 40 45
 Arg Glu Trp Val Lys Phe Ala Lys Pro Cys Arg Glu Gly Glu Asp Asn
 50 55 60
 Ser Lys Arg Asn Pro Ile Ala Lys Ile Thr Ser Asp Tyr Gln Ala Thr
 65 70 75 80
 Gln Lys Ile Thr Tyr Arg Ile Ser Gly Val Gly Ile Asp Gln Pro Pro
 85 90 95
 Phe Gly Ile Phe Val Val Asp Lys Asn Thr Gly Asp Ile Asn Ile Thr
 100 105 110
 Ala Ile Val Asp Arg Glu Glu Thr Pro Ser Phe Leu Ile Thr Cys Arg
 115 120 125
 Ala Leu Asn Ala Gln Gly Leu Asp Val Glu Lys Pro Leu Ile Leu Thr
 130 135 140
 Val Lys Ile Leu Asp Ile Asn Asp Asn Pro Pro Val Phe Ser Gln Gln
 145 150 155 160
 Ile Phe Met Gly Glu Ile Glu Glu Asn Ser Ala Ser Asn Ser Leu Val
 165 170 175
 Met Ile Leu Asn Ala Thr Asp Ala Asp Glu Pro Asn His Leu Asn Ser
 180 185 190
 Lys Ile Ala Phe Lys Ile Val Ser Gln Glu Pro Ala Gly Thr Pro Met
 195 200 205
 Phe Leu Leu Ser Arg Asn Thr Gly Glu Val Arg Thr Leu Thr Asn Ser
 210 215 220
 Leu Asp Arg Glu Gln Ala Ser Ser Tyr Arg Leu Val Val Ser Gly Ala
 225 230 235 240
 Asp Lys Asp Gly Glu Gly Leu Ser Thr Gln Cys Glu Cys Asn Ile Lys
 245 250 255

Val Lys Asp Val Asn Asp Asn Phe Pro Met Phe Arg Asp Ser Gln Tyr
 260 265 270

Ser Ala Arg Ile Glu Glu Asn Ile Leu Ser Ser Glu Leu Leu Arg Phe
 275 280 285

Gln Val Thr Asp Leu Asp Glu Glu Tyr Thr Asp Asn Trp Leu Ala Val
 290 295 300

Tyr Phe Phe Thr Ser Gly Asn Glu Gly Asn Trp Phe Glu Ile Gln Thr
 305 310 315 320

Asp Pro Arg Thr Asn Glu Gly Ile Leu Lys Val Val Lys Ala Leu Asp
 325 330 335

Tyr Glu Gln Leu Gln Ser Val Lys Leu Ser Ile Ala Val Lys Asn Lys
 340 345 350

Ala Glu Phe His Gln Ser Val Ile Ser Arg Tyr Arg Val Gln Ser Thr
 355 360 365

Pro Val Thr Ile Gln Val Ile Asn Val Arg Glu Gly Ile Ala Phe Arg
 370 375 380

Pro Ala Ser Lys Thr Phe Thr Val Gln Lys Gly Ile Ser Ser Lys Lys
 385 390 395 400

Leu Val Asp Tyr Ile Leu Gly Thr Tyr Gln Ala Ile Asp Glu Asp Thr
 405 410 415

Asn Lys Ala Ala Ser Asn Val Lys Tyr Val Met Gly Arg Asn Asp Gly
 420 425 430

Gly Tyr Leu Met Ile Asp Ser Lys Thr Ala Glu Ile Lys Phe Val Lys
 435 440 445

Asn Met Asn Arg Asp Ser Thr Phe Ile Val Asn Lys Thr Ile Thr Ala
 450 455 460

Glu Val Leu Ala Ile Asp Glu Tyr Thr Gly Lys Thr Ser Thr Gly Thr
 465 470 475 480

Val Tyr Val Arg Val Pro Asp Phe Asn Asp Asn Cys Pro Thr Ala Val
 485 490 495

Leu Glu Lys Asp Ala Val Cys Ser Ser Ser Pro Ser Val Val Val Ser
 500 505 510

Ala Arg Thr Leu Asn Asn Arg Tyr Thr Gly Pro Tyr Thr Phe Ala Leu
 515 520 525

Glu Asp Gln Pro Val Lys Leu Pro Ala Val Trp Ser Ile Thr Thr Leu
 530 535 540

Asn Ala Thr Ser Ala Leu Leu Arg Ala Gln Glu Gln Ile Pro Pro Gly
 545 550 555 560

Val Tyr His Ile Ser Leu Val Leu Thr Asp Ser Gln Asn Asn Arg Cys
 565 570 575

Glu Met Pro Arg Ser Leu Thr Leu Glu Val Cys Gln Cys Asp Asn Arg
 580 585 590

Gly Ile Cys Gly Thr Ser Tyr Pro Thr Thr Ser Pro Gly Thr Arg Tyr
 595 600 605

Gly Arg Pro His Ser Gly Arg Leu Gly Pro Ala Ala Ile Gly Leu Leu
 610 615 620

Leu Leu Gly Leu Leu Leu Leu Leu Leu Ala Pro Leu Leu Leu Leu Thr
 625 630 635 640

Cys Asp Cys Gly Ala Gly Ser Thr Gly Gly Val Thr Gly Gly Phe Ile
 645 650 655

Pro Val Pro Asp Gly Ser Glu Gly Thr Ile His Gln Trp Gly Ile Glu
 660 665 670

Gly Ala His Pro Glu Asp Lys Glu Ile Thr Asn Ile Cys Val Pro Pro
 675 680 685

Val Thr Ala Asn Gly Ala Asp Phe Met Glu Ser Ser Glu Val Cys Thr
 690 695 700

Asn Thr Tyr Ala Arg Gly Thr Ala Val Glu Gly Thr Ser Gly Met Glu
 705 710 715 720

Met Thr Thr Lys Leu Gly Ala Ala Thr Glu Ser Gly Gly Ala Ala Gly
 725 730 735

Phe Ala Thr Gly Thr Val Ser Gly Ala Ala Ser Gly Phe Gly Ala Ala
 740 745 750

Thr Gly Val Gly Ile Cys Ser Ser Gly Gln Ser Gly Thr Met Arg Thr
 755 760 765

Arg His Ser Thr Gly Gly Thr Asn Lys Asp Tyr Ala Asp Gly Ala Ile
 770 775 780

Ser Met Asn Phe Leu Asp Ser Tyr Phe Ser Gln Lys Ala Phe Ala Cys
 785 790 795 800

Ala Glu Glu Asp Asp Gly Gln Glu Ala Asn Asp Cys Leu Leu Ile Tyr
 805 810 815

Asp Asn Glu Gly Ala Asp Ala Thr Gly Ser Pro Val Gly Ser Val Gly
 820 825 830

Cys Cys Ser Phe Ile Ala Asp Asp Leu Asp Asp Ser Phe Leu Asp Ser
 835 840 845

Leu Gly Pro Lys Phe Lys Lys Leu Ala Glu Ile Ser Leu Gly Val Asp
 850 855 860

Gly Glu Gly Lys Glu Val Gln Pro Pro Ser Lys Asp Ser Gly Tyr Gly
 865 870 875 880

Ile Glu Ser Cys Gly His Pro Ile Glu Val Gln Gln Thr Gly Phe Val
 885 890 895

Lys Cys Gln Thr Leu Ser Gly Ser Gln Gly Ala Ser Ala Leu Ser Ala
 900 905 910

Ser Gly Ser Val Gln Pro Ala Val Ser Ile Pro Asp Pro Leu Gln His
 915 920 925

Gly Asn Tyr Leu Val Thr Glu Thr Tyr Ser Ala Ser Gly Ser Leu Val
 930 935 940

Gln Pro Ser Thr Ala Gly Phe Asp Pro Leu Leu Thr Gln Asn Val Ile
 945 950 955 960

Val Thr Glu Arg Val Ile Cys Pro Ile Ser Ser Val Pro Gly Asn Leu
 965 970 975

Ala Gly Pro Thr Gln Leu Arg Gly Ser His Thr Met Leu Cys Thr Glu
 980 985 990

Asp Pro Cys Ser Arg Leu Ile
 995

<210> 27
 <211> 1667
 <212> DNA
 <213> Homo sapiens

<400> 27
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 acccgtcttg tggcaaagct atttaaagac tacagcagcg tgggtgcggcc agtgggaagac 180
 caccgccagg tcgtggaggt caccgtgggc ctgcagctga tacagctcat caatgtggat 240
 gaagtaaadc agatcgtgac aaccaatgtg cgtctgaaac agcaatgggt ggattacaac 300
 ctaaaaatgga atccagatga ctatggcggt gtgaaaaaaaa ttcacattcc ttcagaaaag 360
 atctggcgcc cagaccttgt tctctataac aatgcagatg gtgactttgc tattgtcaag 420
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 aaaagctact gtgagatcat cgtcacccac tttccctttg atgaacagaa ctgcagcatg 540
 aagctgggca cctggacctc cgacggctct gtcgtggcca tcaaccggga aagcgaccag 600
 ccagacctga gcaacttcat ggagagcggg gagtgggtga tcaaggagtc ccggggctgg 660
 aagcactcgg tgacctattc ctgctgcccc gacacccctt acctggacat cacctaccac 720
 ttcgatcatgc agcgctgccc cctctacttc atcgtcaacg tcatcatccc ctgcctgctc 780
 ttctccttct taactggocct ggtattctac ctgcccacag actcagggga gaagatgact 840
 ctgagcatct ctgtcttact gtctttgact gtgttccttc tggatcatcgt ggagctgac 900

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ccctccacgt ccagtgtgt gcccttgatt ggaaaataca tgctgttcac catgggtgttc 960
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acccatgtca tgcccaactg ggtgcggaag gtttttatcg acactatccc aaatatcatg 1080
tttttctcca caatgaaaag accatccaga gaaaagcaag acaaaaagat ttttacagaa 1140
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tgtctccctg aagagtgaac cctctttagt aaatgaaact aatcact 1667

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<210> 28
<211> 457
<212> PRT
<213> Homo sapiens

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<400> 28

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Met Glu Pro Trp Pro Leu Leu Leu Leu Phe Ser Leu Cys Ser Ala Gly
1          5          10          15

```

```

Leu Val Leu Gly Ser Glu His Glu Thr Arg Leu Val Ala Lys Leu Phe
20          25          30

```

```

Lys Asp Tyr Ser Ser Val Val Arg Pro Val Glu Asp His Arg Gln Val
35          40          45

```

```

Val Glu Val Thr Val Gly Leu Gln Leu Ile Gln Leu Ile Asn Val Asp
50          55          60

```

```

Glu Val Asn Gln Ile Val Thr Thr Asn Val Arg Leu Lys Gln Gln Trp
65          70          75          80

```

```

Val Asp Tyr Asn Leu Lys Trp Asn Pro Asp Asp Tyr Gly Gly Val Lys
85          90          95

```

Lys Ile His Ile Pro Ser Glu Lys Ile Trp Arg Pro Asp Leu Val Leu
 100 105 110

Tyr Asn Asn Ala Asp Gly Asp Phe Ala Ile Val Lys Phe Thr Lys Val
 115 120 125

Leu Leu Gln Tyr Thr Gly His Ile Thr Trp Thr Pro Pro Ala Ile Phe
 130 135 140

Lys Ser Tyr Cys Glu Ile Ile Val Thr His Phe Pro Phe Asp Glu Gln
 145 150 155 160

Asn Cys Ser Met Lys Leu Gly Thr Trp Thr Tyr Asp Gly Ser Val Val
 165 170 175

Ala Ile Asn Pro Glu Ser Asp Gln Pro Asp Leu Ser Asn Phe Met Glu
 180 185 190

Ser Gly Glu Trp Val Ile Lys Glu Ser Arg Gly Trp Lys His Ser Val
 195 200 205

Thr Tyr Ser Cys Cys Pro Asp Thr Pro Tyr Leu Asp Ile Thr Tyr His
 210 215 220

Phe Val Met Gln Arg Leu Pro Leu Tyr Phe Ile Val Asn Val Ile Ile
 225 230 235 240

Pro Cys Leu Leu Phe Ser Phe Leu Thr Gly Leu Val Phe Tyr Leu Pro
 245 250 255

Thr Asp Ser Gly Glu Lys Met Thr Leu Ser Ile Ser Val Leu Leu Ser
 260 265 270

Leu Thr Val Phe Leu Leu Val Ile Val Glu Leu Ile Pro Ser Thr Ser
 275 280 285

Ser Ala Val Pro Leu Ile Gly Lys Tyr Met Leu Phe Thr Met Val Phe
 290 295 300

Val Ile Ala Ser Ile Ile Ile Thr Val Ile Val Ile Asn Thr His His
 305 310 315 320

Arg Ser Pro Ser Thr His Val Met Pro Asn Trp Val Arg Lys Val Phe
325 330 335

Ile Asp Thr Ile Pro Asn Ile Met Phe Phe Ser Thr Met Lys Arg Pro
340 345 350

Ser Arg Glu Lys Gln Asp Lys Lys Ile Phe Thr Glu Asp Ile Asp Ile
355 360 365

Ser Asp Ile Ser Gly Lys Pro Gly Pro Pro Pro Met Gly Phe His Ser
370 375 380

Pro Leu Ile Lys His Pro Glu Val Lys Ser Ala Ile Glu Gly Ile Lys
385 390 395 400

Tyr Ile Ala Glu Thr Met Lys Ser Asp Gln Glu Ser Asn Asn Ala Ala
405 410 415

Ala Glu Trp Lys Tyr Val Ala Met Val Met Asp His Ile Leu Leu Gly
420 425 430

Val Phe Met Leu Val Cys Ile Ile Gly Thr Leu Ala Val Phe Ala Gly
435 440 445

Arg Leu Ile Glu Leu Asn Gln Gln Gly
450 455

<210> 29
<211> 3587
<212> DNA
<213> Homo sapiens

<400> 29
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gccactctt ttcttctccc cggagtgcag tcaagttgac caagaagcgg gcactgtcca 300
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ccctcgtagc ttatcatcaac tcgcgatgca catctccagg aggtcctac ggtcatctct 420

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tcccacatcc tcagtcccgg ggacccttcc caacttgcca gctgaagtct gagctggaca	600
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actcaccaca gccccccagc atcactgaga atgctgccat ggatgctaga gggctacagg 2160
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 cttccagaaa aattggggga gctgcagtc cctgcacaag atgccccagg gatgggaggt 3480
 atgggctggg ggctatgtat agtctgtata cgttttgagg agaaatttga taatgacact 3540
 gtttctgat aataaaggaa ctgcatcaga aaaaaaaaaa aaaaaaa 3587

<210> 30
 <211> 1106
 <212> PRT
 <213> Homo sapiens

<400> 30

Met Phe Asn Ser Met Thr Pro Pro Pro Ile Ser Ser Tyr Gly Glu Pro
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Cys Cys Leu Arg Pro Leu Pro Ser Gln Gly Ala Pro Ser Val Gly Thr
 20 25 30

Glu Gly Leu Ser Gly Pro Pro Phe Cys His Gln Ala Asn Leu Met Ser
 35 40 45

Gly Pro His Ser Tyr Gly Pro Ala Arg Glu Thr Asn Ser Cys Thr Glu
 50 55 60

Gly Pro Leu Phe Ser Ser Pro Arg Ser Ala Val Lys Leu Thr Lys Lys
 65 70 75 80

Arg Ala Leu Ser Ile Ser Pro Leu Ser Asp Ala Ser Leu Asp Leu Gln
 85 90 95

Thr Val Ile Arg Thr Ser Pro Ser Ser Leu Val Ala Phe Ile Asn Ser
 100 105 110

Arg Cys Thr Ser Pro Gly Gly Ser Tyr Gly His Leu Ser Ile Gly Thr
 115 120 125

Met Ser Pro Ser Leu Gly Phe Pro Ala Gln Met Asn His Gln Lys Gly
 130 135 140

Pro Ser Pro Ser Phe Gly Val Gln Pro Cys Gly Pro His Asp Ser Ala
 145 150 155 160

Arg Gly Gly Met Ile Pro His Pro Gln Ser Arg Gly Pro Phe Pro Thr
 165 170 175

Cys Gln Leu Lys Ser Glu Leu Asp Met Leu Val Gly Lys Cys Arg Glu
 180 185 190

Glu Pro Leu Glu Gly Asp Met Ser Ser Pro Asn Ser Thr Gly Ile Gln
 195 200 205

Asp Pro Leu Leu Gly Met Leu Asp Gly Arg Glu Asp Leu Glu Arg Glu
 210 215 220

Glu Lys Arg Glu Pro Glu Ser Val Tyr Glu Thr Asp Cys Arg Trp Asp
 225 230 235 240

Gly Cys Ser Gln Glu Phe Asp Ser Gln Glu Gln Leu Val His His Ile
 245 250 255

Asn Ser Glu His Ile His Gly Glu Arg Lys Glu Phe Val Cys His Trp
 260 265 270

Gly Gly Cys Ser Arg Glu Leu Arg Pro Phe Lys Ala Gln Tyr Met Leu
 275 280 285

Val Val His Met Arg Arg His Thr Gly Glu Lys Pro His Lys Cys Thr
 290 295 300

Phe Glu Gly Cys Arg Lys Ser Tyr Ser Arg Leu Glu Asn Leu Lys Thr
 305 310 315 320

His Leu Arg Ser His Thr Gly Glu Lys Pro Tyr Met Cys Glu His Glu
 325 330 335

Gly Cys Ser Lys Ala Phe Ser Asn Ala Ser Asp Arg Ala Lys His Gln
 340 345 350

Asn Arg Thr His Ser Asn Glu Lys Pro Tyr Val Cys Lys Leu Pro Gly
 355 360 365

Cys Thr Lys Arg Tyr Thr Asp Pro Ser Ser Leu Arg Lys His Val Lys
 370 375 380

Thr Val His Gly Pro Asp Ala His Val Thr Lys Arg His Arg Gly Asp
 385 390 395 400

Gly Pro Leu Pro Arg Ala Pro Ser Ile Ser Thr Val Glu Pro Lys Arg
 405 410 415

Glu Arg Glu Gly Gly Pro Ile Arg Glu Glu Ser Arg Leu Thr Val Pro
 420 425 430

Glu Gly Ala Met Lys Pro Gln Pro Ser Pro Gly Ala Gln Ser Ser Cys
 435 440 445

Ser Ser Asp His Ser Pro Ala Gly Ser Ala Ala Asn Thr Asp Ser Gly
 450 455 460

Val Glu Met Thr Gly Asn Ala Gly Gly Ser Thr Glu Asp Leu Ser Ser
 465 470 475 480

Leu Asp Glu Gly Pro Cys Ile Ala Gly Thr Gly Leu Ser Thr Leu Arg
 485 490 495

Arg Leu Glu Asn Leu Arg Leu Asp Gln Leu His Gln Leu Arg Pro Ile
 500 505 510

Gly Thr Arg Gly Leu Lys Leu Pro Ser Leu Ser His Thr Gly Thr Thr
 515 520 525

Val Ser Arg Arg Val Gly Pro Pro Val Ser Leu Glu Arg Arg Ser Ser
 530 535 540

Ser Ser Ser Ser Ile Ser Ser Ala Tyr Thr Val Ser Arg Arg Ser Ser
 545 550 555 560

Leu Ala Ser Pro Phe Pro Pro Gly Ser Pro Pro Glu Asn Gly Ala Ser
 565 570 575

Ser Leu Pro Gly Leu Met Pro Ala Gln His Tyr Leu Leu Arg Ala Arg
 580 585 590

Tyr Ala Ser Ala Arg Gly Gly Gly Thr Ser Pro Thr Ala Ala Ser Ser
 595 600 605

Leu Asp Arg Ile Gly Gly Leu Pro Met Pro Pro Trp Arg Ser Arg Ala
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Glu Tyr Pro Gly Tyr Asn Pro Asn Ala Gly Val Thr Arg Arg Ala Ser
 625 630 635 640

Asp Pro Ala Gln Ala Ala Asp Arg Pro Ala Pro Ala Arg Val Gln Arg
 645 650 655

Phe Lys Ser Leu Gly Cys Val His Thr Pro Pro Thr Val Ala Gly Gly
 660 665 670

Gly Gln Asn Phe Asp Pro Tyr Leu Pro Thr Ser Val Tyr Ser Pro Gln
 675 680 685

Pro Pro Ser Ile Thr Glu Asn Ala Ala Met Asp Ala Arg Gly Leu Gln
 690 695 700

Glu Glu Pro Glu Val Gly Thr Ser Met Val Gly Ser Gly Leu Asn Pro
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Tyr Met Asp Phe Pro Pro Thr Asp Thr Leu Gly Tyr Gly Gly Pro Glu
 725 730 735

Gly Ala Ala Ala Glu Pro Tyr Gly Ala Arg Gly Pro Gly Ser Leu Pro
 740 745 750

Leu Gly Pro Gly Pro Pro Thr Asn Tyr Gly Pro Asn Pro Cys Pro Gln
 755 760 765

Gln Ala Ser Tyr Pro Asp Pro Thr Gln Glu Thr Trp Gly Glu Phe Pro
 770 775 780

Ser His Ser Gly Leu Tyr Pro Gly Pro Lys Ala Leu Gly Gly Thr Tyr
 785 790 795 800

Ser Gln Cys Pro Arg Leu Glu His Tyr Gly Gln Val Gln Val Lys Pro
 805 810 815

Glu Gln Gly Cys Pro Val Gly Ser Asp Ser Thr Gly Leu Ala Pro Cys
 820 825 830

Leu Asn Ala His Pro Ser Glu Gly Pro Pro His Pro Gln Pro Leu Phe
 835 840 845

Ser His Tyr Pro Gln Pro Ser Pro Pro Gln Tyr Leu Gln Ser Gly Pro
 850 855 860

Tyr Thr Gln Pro Pro Pro Asp Tyr Leu Pro Ser Glu Pro Arg Pro Cys
 865 870 875 880

Leu Asp Phe Asp Ser Pro Thr His Ser Thr Gly Gln Leu Lys Ala Gln
 885 890 895

Leu Val Cys Asn Tyr Val Gln Ser Gln Gln Glu Leu Leu Trp Glu Gly
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Gly Gly Arg Glu Asp Ala Pro Ala Gln Glu Pro Ser Tyr Gln Ser Pro
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Lys Phe Leu Gly Gly Ser Gln Val Ser Pro Ser Arg Ala Lys Ala Pro
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Val Asn Thr Tyr Gly Pro Gly Phe Gly Pro Asn Leu Pro Asn His Lys
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Ser Gly Ser Tyr Pro Thr Pro Ser Pro Cys His Glu Asn Phe Val Val
 965 970 975

Gly Ala Asn Arg Ala Ser His Arg Ala Ala Ala Pro Pro Arg Leu Leu
 980 985 990

Pro Pro Leu Pro Thr Cys Tyr Gly Pro Leu Lys Val Gly Gly Thr Asn
 995 1000 1005

Pro Ser Cys Gly His Pro Glu Val Gly Arg Leu Gly Gly Gly Pro
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Ala Leu Tyr Pro Pro Pro Glu Gly Gln Val Cys Asn Pro Leu Asp
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Ser Leu Asp Leu Asp Asn Thr Gln Leu Asp Phe Val Ala Ile Leu
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Asp Glu Pro Gln Gly Leu Ser Pro Pro Pro Ser His Asp Gln Arg
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Gly Ser Ser Gly His Thr Pro Pro Pro Ser Gly Pro Pro Asn Met
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Ala Val Gly Asn Met Ser Val Leu Leu Arg Ser Leu Pro Gly Glu
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Thr Glu Phe Leu Asn Ser Ser Ala
 1100 1105

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 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 32

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Ala Arg Lys Arg Lys Arg Thr Ser Ile Glu Asn Arg Val Arg Gly Asn
35 40 45

Leu Glu Asn Leu Phe Leu Gln Cys Pro Lys Pro Thr Leu Gln Gln Ile
50 55 60

Ser His Ile Ala Gln Gln Leu Gly Leu Glu Lys Asp Val Val Arg Val
65 70 75 80

Trp Phe Cys Asn Arg Arg Gln Lys Gly Lys Arg Ser Ser Ser Asp Tyr
85 90 95

Ala Gln Arg Glu Asp Phe Glu Ala Ala Gly Ser Pro Phe Ser Gly Gly
100 105 110

Pro Val Ser Phe Pro Leu Ala Pro Gly Pro His Phe Gly Thr Pro Gly
115 120 125

Tyr Gly Ser Pro His Phe Thr Ala Leu Tyr Ser Ser Val Pro Phe Pro
130 135 140

Glu Gly Glu Ala Phe Pro Pro Val Ser Val Thr Thr Leu Gly Ser Pro
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Met His Ser Asn

<210> 33

<211> 2130

<212> DNA

<213> Homo sapiens

<400> 33

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 <212> PRT
 <213> Homo sapiens

<400> 34

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Asn Thr Phe Asp Leu Val Ala Leu Gly Val Gly Ser Thr Leu Gly Ala
 35 40 45

Gly Val Tyr Val Leu Ala Gly Ala Val Ala Arg Glu Asn Ala Gly Pro
 50 55 60

Ala Ile Val Ile Ser Phe Leu Ile Ala Ala Leu Ala Ser Val Leu Ala
 65 70 75 80

Gly Leu Cys Tyr Gly Glu Phe Gly Ala Arg Val Pro Lys Thr Gly Ser
 85 90 95

Ala Tyr Leu Tyr Ser Tyr Val Thr Val Gly Glu Leu Trp Ala Phe Ile
 100 105 110

Thr Gly Trp Asn Leu Ile Leu Ser Tyr Ile Ile Gly Thr Ser Ser Val
 115 120 125

Ala Arg Ala Trp Ser Ala Thr Phe Asp Glu Leu Ile Gly Arg Pro Ile
 130 135 140

Gly Glu Phe Ser Arg Thr His Met Thr Leu Asn Ala Pro Gly Val Leu
 145 150 155 160

Ala Glu Asn Pro Asp Ile Phe Ala Val Ile Ile Ile Leu Ile Leu Thr
 165 170 175

Gly Leu Leu Thr Leu Gly Val Lys Glu Ser Ala Met Val Asn Lys Ile
 180 185 190

Phe Thr Cys Ile Asn Val Leu Val Leu Gly Phe Ile Met Val Ser Gly
 195 200 205

Phe Val Lys Gly Ser Val Lys Asn Trp Gln Leu Thr Glu Glu Asp Phe
 210 215 220

Gly Asn Thr Ser Gly Arg Leu Cys Leu Asn Asn Asp Thr Lys Glu Gly
 225 230 235 240

Lys Pro Gly Val Gly Gly Phe Met Pro Phe Gly Phe Ser Gly Val Leu
 245 250 255

Ser Gly Ala Ala Thr Cys Phe Tyr Ala Phe Val Gly Phe Asp Cys Ile
 260 265 270

Ala Thr Thr Gly Glu Glu Val Lys Asn Pro Gln Lys Ala Ile Pro Val
 275 280 285

Gly Ile Val Ala Ser Leu Leu Ile Cys Phe Ile Ala Tyr Phe Gly Val
 290 295 300

Ser Ala Ala Leu Thr Leu Met Met Pro Tyr Phe Cys Leu Asp Asn Asn
 305 310 315 320

Ser Pro Leu Pro Asp Ala Phe Lys His Val Gly Trp Glu Gly Ala Lys
 325 330 335

Tyr Ala Val Ala Val Gly Ser Leu Cys Ala Leu Ser Ala Ser Leu Leu
 340 345 350

Gly Ser Met Phe Pro Met Pro Arg Val Ile Tyr Ala Met Ala Glu Asp
 355 360 365

Gly Leu Leu Phe Lys Phe Leu Ala Asn Val Asn Asp Arg Thr Lys Thr
 370 375 380

Pro Ile Ile Ala Thr Leu Ala Ser Gly Ala Val Ala Ala Val Met Ala
 385 390 395 400

Phe Leu Phe Asp Leu Lys Asp Leu Val Asp Leu Met Ser Ile Gly Thr
 405 410 415

Leu Leu Ala Tyr Ser Leu Val Ala Ala Cys Val Leu Val Leu Arg Tyr
 420 425 430

Gln Pro Glu Gln Pro Asn Leu Val Tyr Gln Met Ala Ser Thr Ser Asp
 435 440 445

Glu Leu Asp Pro Ala Asp Gln Asn Glu Leu Ala Ser Thr Asn Asp Ser
 450 455 460

Gln Leu Gly Phe Leu Pro Glu Ala Glu Met Phe Ser Leu Lys Thr Ile
 465 470 475 480

Leu Ser Pro Lys Asn Met Glu Pro Ser Lys Ile Ser Gly Leu Ile Val
 485 490 495

Asn Ile Ser Thr Ser Leu Ile Ala Val Leu Ile Ile Thr Phe Cys Ile
 500 505 510

Val Thr Val Leu Gly Arg Glu Ala Leu Thr Lys Gly Ala Leu Trp Ala
 515 520 525

Val Phe Leu Leu Ala Gly Ser Ala Leu Leu Cys Ala Val Val Thr Gly
 530 535 540

Val Ile Trp Arg Gln Pro Glu Ser Lys Thr Lys Leu Ser Phe Lys Val
 545 550 555 560

Pro Phe Leu Pro Val Leu Pro Ile Leu Ser Ile Phe Val Asn Val Tyr
 565 570 575

Leu Met Met Gln Leu Asp Gln Gly Thr Trp Val Arg Phe Ala Val Trp
 580 585 590

Met Leu Ile Gly Phe Ile Ile Tyr Phe Gly Tyr Gly Leu Trp His Ser
 595 600 605

Glu Glu Ala Ser Leu Asp Ala Asp Gln Ala Arg Thr Pro Asp Gly Asn
 610 615 620

Leu Asp Gln Cys Lys
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<212> DNA
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<210> 36
<211> 573
<212> PRT
<213> Homo sapiens

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<400> 36

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Met Leu Glu Asn Tyr Gln Asn Leu Leu Ala Leu Gly Pro Pro Leu His
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Lys Pro Asp Val Ile Ser His Leu Glu Arg Gly Glu Glu Pro Trp Ser
20          25          30

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Met Gln Arg Glu Val Pro Arg Gly Pro Cys Pro Glu Trp Glu Leu Lys
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 Ala Val Pro Ser Gln Gln Gln Gly Ile Cys Lys Glu Glu Pro Ala Gln
 50 55 60
 Glu Pro Ile Met Glu Arg Pro Leu Gly Gly Ala Gln Ala Trp Gly Arg
 65 70 75 80
 Gln Ala Gly Ala Leu Gln Arg Ser Gln Ala Ala Pro Trp Ala Pro Ala
 85 90 95
 Pro Ala Met Val Trp Asp Val Pro Val Glu Glu Phe Pro Leu Arg Cys
 100 105 110
 Pro Leu Phe Ala Gln Gln Arg Val Pro Glu Gly Gly Pro Leu Leu Asp
 115 120 125
 Thr Arg Lys Asn Val Gln Ala Thr Glu Gly Arg Thr Lys Ala Pro Ala
 130 135 140
 Arg Leu Cys Ala Gly Glu Asn Ala Ser Thr Pro Ser Glu Pro Glu Lys
 145 150 155 160
 Phe Pro Gln Val Arg Arg Gln Arg Gly Ala Gly Ala Gly Glu Gly Glu
 165 170 175
 Phe Val Cys Gly Glu Cys Gly Lys Ala Phe Arg Gln Ser Ser Ser Leu
 180 185 190
 Thr Leu His Arg Arg Trp His Ser Arg Glu Lys Ala Tyr Lys Cys Asp
 195 200 205
 Glu Cys Gly Lys Ala Phe Thr Trp Ser Thr Asn Leu Leu Glu His Arg
 210 215 220
 Arg Ile His Thr Gly Glu Lys Pro Phe Phe Cys Gly Glu Cys Gly Lys
 225 230 235 240
 Ala Phe Ser Cys His Ser Ser Leu Asn Val His Gln Arg Ile His Thr
 245 250 255

Gly Glu Arg Pro Tyr Lys Cys Ser Ala Cys Glu Lys Ala Phe Ser Cys
 260 265 270

Ser Ser Leu Leu Ser Met His Leu Arg Val His Thr Gly Glu Lys Pro
 275 280 285

Tyr Arg Cys Gly Glu Cys Gly Lys Ala Phe Asn Gln Arg Thr His Leu
 290 295 300

Thr Arg His His Arg Ile His Thr Gly Glu Lys Pro Tyr Gln Cys Gly
 305 310 315 320

Ser Cys Gly Lys Ala Phe Thr Cys His Ser Ser Leu Thr Val His Glu
 325 330 335

Lys Ile His Ser Gly Asp Lys Pro Phe Lys Cys Ser Asp Cys Glu Lys
 340 345 350

Ala Phe Asn Ser Arg Ser Arg Leu Thr Leu His Gln Arg Thr His Thr
 355 360 365

Gly Glu Lys Pro Phe Lys Cys Ala Asp Cys Gly Lys Gly Phe Ser Cys
 370 375 380

His Ala Tyr Leu Leu Val His Arg Arg Ile His Ser Gly Glu Lys Pro
 385 390 395 400

Phe Lys Cys Asn Glu Cys Gly Lys Ala Phe Ser Ser His Ala Tyr Leu
 405 410 415

Ile Val His Arg Arg Ile His Thr Gly Glu Lys Pro Phe Asp Cys Ser
 420 425 430

Gln Cys Trp Lys Ala Phe Ser Cys His Ser Ser Leu Ile Val His Gln
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Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Ser Glu Cys Gly Arg
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Ala Phe Ser Gln Asn His Cys Leu Ile Lys His Gln Lys Ile His Ser
 465 470 475 480

Gly Glu Lys Ser Phe Lys Cys Glu Lys Cys Gly Glu Met Phe Asn Trp
 485 490 495

Ser Ser His Leu Thr Glu His Gln Arg Leu His Ser Glu Gly Lys Pro
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Leu Ala Ile Gln Phe Asn Lys His Leu Leu Ser Thr Tyr Tyr Val Pro
 515 520 525

Gly Ser Leu Leu Gly Ala Gly Asp Ala Gly Leu Arg Asp Val Asp Pro
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Ile Asp Ala Leu Asp Val Ala Lys Leu Leu Cys Val Val Pro Pro Arg
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 <212> DNA
 <213> Homo sapiens

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Gln Ala Met Asn Val Ala Leu Asn Thr Cys Ser Tyr Asn Ser Ile Leu
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Ser Ile Thr Val Gln Glu Pro Gly Leu Pro Gly Thr Ser Thr Leu Leu
115 120 125

Phe Gln Cys Gln Glu Val Gly Ala Glu Arg Leu Lys Thr Ser Leu Gln
130 135 140

Lys Ala Leu Glu Glu Glu Leu Glu Gln Ser Arg Pro Arg Leu Gly Gly
145 150 155 160

Leu Gln Pro Gly Gln Asp Arg Trp Arg Gly Pro Ala Met Glu Arg Pro
165 170 175

Leu Pro Met Glu Gln Ala Arg Tyr Leu Glu Pro Gly Ile Pro Pro Glu
180 185 190

Gln Pro His Gln Arg Thr Leu Glu His Ser Leu Pro Pro Ser Pro Arg
195 200 205

Pro Leu Pro Arg His Thr Ser Ala Arg Glu Pro Ser Ala Phe Thr Leu
210 215 220

Pro Pro Pro Arg Arg Ser Ser Ser Pro Glu Asp Pro Glu Arg Asp Glu
225 230 235 240

Glu Val Leu Asn His Val Leu Arg Asp Ile Glu Leu Phe Met Gly Lys
245 250 255

Leu Glu Lys Ala Gln Ala Lys Thr Ser Arg Lys Lys Lys Phe Gly Lys
260 265 270

Lys Asn Lys Asp Gln Gly Gly Leu Thr Gln Ala Gln Tyr Ile Asp Cys
275 280 285

Phe Gln Lys Ile Lys Tyr Ser Phe Asn Leu Leu Gly Arg Leu Ala Thr
 290 295 300

Trp Leu Lys Glu Thr Ser Ala Pro Glu Leu Val His Ile Leu Phe Lys
 305 310 315 320

Ser Leu Asn Phe Ile Leu Ala Arg Cys Pro Glu Ala Gly Leu Ala Ala
 325 330 335

Gln Val Ile Ser Pro Leu Leu Thr Pro Lys Ala Ile Asn Leu Leu Gln
 340 345 350

Ser Cys Leu Ser Pro Pro Glu Ser Asn Leu Trp Met Gly Leu Gly Pro
 355 360 365

Ala Trp Thr Thr Ser Arg Ala Asp Trp Thr Gly Asp Glu Pro Leu Pro
 370 375 380

Tyr Gln Pro Thr Phe Ser Asp Asp Trp Gln Leu Pro Glu Pro Ser Ser
 385 390 395 400

Gln Ala Pro Leu Gly Tyr Gln Asp Pro Val Ser Leu Arg Arg Gly Ser
 405 410 415

His Arg Leu Gly Ser Thr Ser His Phe Pro Gln Glu Lys Thr His Asn
 420 425 430

His Asp Pro Gln Pro Gly Asp Pro Asn Ser Arg Pro Ser Ser Pro Lys
 435 440 445

Pro Ala Gln Pro Ala Leu Lys Met Gln Val Leu Tyr Glu Phe Glu Ala
 450 455 460

Arg Asn Pro Arg Glu Leu Thr Val Val Gln Gly Glu Lys Leu Glu Val
 465 470 475 480

Leu Asp His Ser Lys Arg Trp Trp Leu Val Lys Asn Glu Ala Gly Arg
 485 490 495

Ser Gly Tyr Ile Pro Ser Asn Ile Leu Glu Pro Leu Gln Pro Gly Thr
 500 505 510

Pro Gly Thr Gln Gly Gln Ser Pro Ser Arg Val Pro Met Leu Arg Leu
515 520 525

Ser Ser Arg Pro Glu Glu Val Thr Asp Trp Leu Gln Ala Glu Asn Phe
530 535 540

Ser Thr Ala Thr Val Arg Thr Leu Gly Ser Leu Thr Gly Ser Gln Leu
545 550 555 560

Leu Arg Ile Arg Pro Gly Glu Leu Gln Met Leu Cys Pro Gln Glu Ala
565 570 575

Pro Arg Ile Leu Ser Arg Leu Glu Ala Val Arg Arg Met Leu Gly Ile
580 585 590

Ser Pro

<210> 41
<211> 3600
<212> DNA
<213> Homo sapiens

<400> 41
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tcaacttaaa ggtgtatcca tgttgtagca cgtgtcagca ttttctttcg ttctcaggct 120
aaatagtatt tcattgtgtg tgtacaccat gtttcatgca ttcatcctc ccttgaaaga 180
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ctgcgccccat gagtgagctt gtgcctgacc tctccttcca ggtggactta cacactgggc 720
tgtcggagtt ctcggtgacg cagcgccggc tggcccatgg ctggaatgag tttgttgctg 780

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<210> 42
 <211> 963
 <212> PRT
 <213> Homo sapiens

<400> 42

Met Leu His Phe His Leu Leu Lys Phe Lys Thr Arg Val Ile Phe Ser
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Ala Val Ile Ile Met Val Thr Gly Leu Cys Leu Phe Leu Leu Ser Leu
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Pro His Leu His Gly Val Phe Glu Gln Val Pro Ala Pro Trp Trp Thr
 35 40 45

Ser Leu Cys Pro Trp Pro Ile Met Glu Ala Ala Ala Phe Gln Ser Gly
 50 55 60

Ser Leu Tyr Pro Val Ala Ser Phe Leu Ala Ala Pro Met Ser Glu Leu
 65 70 75 80

Val Pro Asp Leu Ser Phe Gln Val Asp Leu His Thr Gly Leu Ser Glu
 85 90 95

Phe Ser Val Thr Gln Arg Arg Leu Ala His Gly Trp Asn Glu Phe Val
 100 105 110

Ala Asp Asn Ser Glu Pro Val Trp Lys Lys Tyr Leu Asp Gln Phe Lys
 115 120 125

Asn Pro Leu Ile Leu Leu Leu Leu Gly Ser Ala Leu Val Ser Val Leu
 130 135 140

Thr Lys Glu Tyr Glu Asp Ala Val Ser Ile Ala Thr Ala Val Leu Val
 145 150 155 160

Val Val Thr Val Ala Phe Ile Gln Glu Tyr Arg Ser Glu Lys Ser Leu
 165 170 175

Glu Glu Leu Thr Lys Leu Val Pro Pro Glu Cys Asn Cys Leu Arg Glu
 180 185 190

Gly Lys Leu Gln His Leu Leu Ala Arg Glu Leu Val Pro Gly Asp Val
 195 200 205

Val Ser Leu Ser Ile Gly Asp Arg Ile Pro Ala Asp Ile Arg Leu Thr
 210 215 220

Glu Val Thr Asp Leu Leu Val Asp Glu Ser Ser Phe Thr Gly Glu Ala
 225 230 235 240

Glu Pro Cys Ser Lys Thr Asp Ser Pro Leu Thr Gly Gly Gly Asp Leu
 245 250 255

Thr Thr Leu Ser Asn Ile Val Phe Met Gly Thr Leu Val Gln Tyr Gly
 260 265 270

Arg Gly Gln Gly Val Val Ile Gly Thr Gly Glu Ser Ser Gln Phe Gly
 275 280 285

Glu Val Phe Lys Met Met Gln Ala Glu Glu Thr Pro Lys Thr Pro Leu
 290 295 300

Gln Lys Ser Met Asp Arg Leu Gly Lys Gln Leu Thr Leu Phe Ser Phe
 305 310 315 320

Gly Ile Ile Gly Leu Ile Met Leu Ile Gly Trp Ser Gln Gly Lys Gln
 325 330 335

Leu Leu Ser Met Phe Thr Ile Gly Val Ser Leu Ala Val Ala Ala Ile
 340 345 350

Pro Glu Gly Leu Pro Ile Val Val Met Val Thr Leu Val Leu Gly Val
 355 360 365

Leu Arg Met Ala Lys Lys Arg Val Ile Val Lys Lys Leu Pro Ile Val
 370 375 380

Glu Thr Leu Gly Cys Cys Ser Val Leu Cys Ser Asp Lys Thr Gly Thr
 385 390 395 400

Leu Thr Ala Asn Glu Met Thr Val Thr Gln Leu Val Thr Ser Asp Gly
 405 410 415

Leu Arg Ala Glu Val Ser Gly Val Gly Tyr Asp Gly Gln Gly Thr Val
 420 425 430

Cys Leu Leu Pro Ser Lys Glu Val Ile Lys Glu Phe Ser Asn Val Ser
 435 440 445

Val Gly Lys Leu Val Glu Ala Gly Cys Val Ala Asn Asn Ala Val Ile
 450 455 460

Arg Lys Asn Ala Val Met Gly Gln Pro Thr Glu Gly Ala Leu Met Ala
 465 470 475 480

Leu Ala Met Lys Met Asp Leu Ser Asp Ile Lys Asn Ser Tyr Ile Arg
 485 490 495

Lys Lys Glu Ile Pro Phe Ser Ser Glu Gln Lys Trp Met Ala Val Lys
 500 505 510

Cys Ser Leu Lys Thr Glu Asp Gln Glu Asp Ile Tyr Phe Met Lys Gly
 515 520 525

Ala Leu Glu Glu Val Ile Arg Tyr Cys Thr Met Tyr Asn Asn Gly Gly
 530 535 540

Ile Pro Leu Pro Leu Thr Pro Gln Gln Arg Ser Phe Cys Leu Gln Glu
 545 550 555 560

Glu Lys Arg Met Gly Ser Leu Gly Leu Arg Val Leu Ala Leu Ala Ser
 565 570 575

Gly Pro Glu Leu Gly Arg Leu Thr Phe Leu Gly Leu Val Gly Ile Ile
 580 585 590

Asp Pro Pro Arg Val Gly Val Lys Glu Ala Val Gln Val Leu Ser Glu
 595 600 605

Ser Gly Val Ser Val Lys Met Ile Thr Gly Asp Ala Leu Glu Thr Ala
 610 615 620

Leu Ala Ile Gly Arg Asn Ile Gly Leu Cys Asn Gly Lys Leu Gln Ala
 625 630 635 640

Met Ser Gly Glu Glu Val Asp Ser Val Glu Lys Gly Glu Leu Ala Asp
 645 650 655

Arg Val Gly Lys Val Ser Val Phe Phe Arg Thr Ser Pro Lys His Lys
 660 665 670

Leu Lys Ile Ile Lys Ala Leu Gln Glu Ser Gly Ala Ile Val Ala Met
 675 680 685

Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ser Ala Asp Ile
 690 695 700

Gly Ile Ala Met Gly Gln Thr Gly Thr Asp Val Ser Lys Glu Ala Ala
 705 710 715 720

Asn Met Ile Leu Val Asp Asp Asp Phe Ser Ala Ile Met Asn Ala Val
 725 730 735

Glu Glu Gly Lys Gly Ile Phe Tyr Asn Ile Lys Asn Phe Val Arg Phe
 740 745 750

Gln Leu Ser Thr Ser Ile Ser Ala Leu Ser Leu Ile Thr Leu Ser Thr
 755 760 765

Val Phe Asn Leu Pro Ser Pro Leu Asn Ala Met Gln Ile Leu Trp Ile
 770 775 780

Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly Val Glu Pro
 785 790 795 800

Val Asp Lys Asp Ala Phe Arg Gln Pro Pro Arg Ser Val Arg Asp Thr
 805 810 815

Ile Leu Ser Arg Ala Leu Ile Leu Lys Ile Leu Met Ser Ala Ala Ile
 820 825 830

Ile Ile Ser Gly Thr Leu Phe Ile Phe Trp Lys Glu Met Pro Glu Asp
 835 840 845

Arg Ala Ser Thr Pro Arg Thr Thr Thr Met Thr Phe Thr Cys Phe Val
 850 855 860

Phe Phe Asp Leu Phe Asn Ala Leu Thr Cys Arg Ser Gln Thr Lys Leu
 865 870 875 880

Ile Phe Glu Ile Gly Phe Leu Arg Asn His Met Phe Leu Tyr Ser Val
 885 890 895

Leu Gly Ser Ile Leu Gly Gln Leu Ala Val Ile Tyr Ile Pro Pro Leu
 900 905 910

Gln Arg Val Phe Gln Thr Glu Asn Leu Gly Ala Leu Asp Leu Leu Phe
 915 920 925

Leu Thr Gly Leu Ala Ser Ser Val Phe Ile Leu Ser Glu Leu Leu Lys
 930 935 940

Leu Cys Glu Lys Tyr Cys Cys Ser Pro Lys Arg Val Gln Met His Pro
 945 950 955 960

Glu Asp Val

<210> 43
 <211> 2076
 <212> DNA
 <213> Homo sapiens

<400> 43
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ataaagagaa gcaatgtgaa aaaaaaaaaa aaaaaa 2076

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<210> 44
<211> 509
<212> PRT
<213> Homo sapiens

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<400> 44

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Met Glu Arg Arg Arg Leu Trp Gly Ser Ile Gln Ser Arg Tyr Ile Ser
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Met Ser Val Trp Thr Ser Pro Arg Arg Leu Val Glu Leu Ala Gly Gln
20           25           30

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Ser Leu Leu Lys Asp Glu Ala Leu Ala Ile Ala Ala Leu Glu Leu Leu
35           40           45

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Pro Arg Glu Leu Phe Pro Pro Leu Phe Met Ala Ala Phe Asp Gly Arg
50           55           60

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His Ser Gln Thr Leu Lys Ala Met Val Gln Ala Trp Pro Phe Thr Cys
65           70           75           80

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Leu Pro Leu Gly Val Leu Met Lys Gly Gln His Leu His Leu Glu Thr
 85 90 95

Phe Lys Ala Val Leu Asp Gly Leu Asp Val Leu Leu Ala Gln Glu Val
 100 105 110

Arg Pro Arg Arg Trp Lys Leu Gln Val Leu Asp Leu Arg Lys Asn Ser
 115 120 125

His Gln Asp Phe Trp Thr Val Trp Ser Gly Asn Arg Ala Ser Leu Tyr
 130 135 140

Ser Phe Pro Glu Pro Glu Ala Ala Gln Pro Met Thr Lys Lys Arg Lys
 145 150 155 160

Val Asp Gly Leu Ser Thr Glu Ala Glu Gln Pro Phe Ile Pro Val Glu
 165 170 175

Val Leu Val Asp Leu Phe Leu Lys Glu Gly Ala Cys Asp Glu Leu Phe
 180 185 190

Ser Tyr Leu Ile Glu Lys Val Lys Arg Lys Lys Asn Val Leu Arg Leu
 195 200 205

Cys Cys Lys Lys Leu Lys Ile Phe Ala Met Pro Met Gln Asp Ile Lys
 210 215 220

Met Ile Leu Lys Met Val Gln Leu Asp Ser Ile Glu Asp Leu Glu Val
 225 230 235 240

Thr Cys Thr Trp Lys Leu Pro Thr Leu Ala Lys Phe Ser Pro Tyr Leu
 245 250 255

Gly Gln Met Ile Asn Leu Arg Arg Leu Leu Leu Ser His Ile His Ala
 260 265 270

Ser Ser Tyr Ile Ser Pro Glu Lys Glu Glu Gln Tyr Ile Ala Gln Phe
 275 280 285

Thr Ser Gln Phe Leu Ser Leu Gln Cys Leu Gln Ala Leu Tyr Val Asp
 290 295 300

Ser Leu Phe Phe Leu Arg Gly Arg Leu Asp Gln Leu Leu Arg His Val
305 310 315 320

Met Asn Pro Leu Glu Thr Leu Ser Ile Thr Asn Cys Arg Leu Ser Glu
325 330 335

Gly Asp Val Met His Leu Ser Gln Ser Pro Ser Val Ser Gln Leu Ser
340 345 350

Val Leu Ser Leu Ser Gly Val Met Leu Thr Asp Val Ser Pro Glu Pro
355 360 365

Leu Gln Ala Leu Leu Glu Arg Ala Ser Ala Thr Leu Gln Asp Leu Val
370 375 380

Phe Asp Glu Cys Gly Ile Thr Asp Asp Gln Leu Leu Ala Leu Leu Pro
385 390 395 400

Ser Leu Ser His Cys Ser Gln Leu Thr Thr Leu Ser Phe Tyr Gly Asn
405 410 415

Ser Ile Ser Ile Ser Ala Leu Gln Ser Leu Leu Gln His Leu Ile Gly
420 425 430

Leu Ser Asn Leu Thr His Val Leu Tyr Pro Val Pro Leu Glu Ser Tyr
435 440 445

Glu Asp Ile His Gly Thr Leu His Leu Glu Arg Leu Ala Tyr Leu His
450 455 460

Ala Arg Leu Arg Glu Leu Leu Cys Glu Leu Gly Arg Pro Ser Met Val
465 470 475 480

Trp Leu Ser Ala Asn Pro Cys Pro His Cys Gly Asp Arg Thr Phe Tyr
485 490 495

Asp Pro Glu Pro Ile Leu Cys Pro Cys Phe Met Pro Asn
500 505

<210> 45
<211> 1445
<212> DNA
<213> Homo sapiens

<400> 45
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 ccaa 1445

<210> 46
 <211> 297
 <212> PRT
 <213> Homo sapiens

<400> 46

Met Thr Met Glu Ser Arg Glu Met Asp Cys Tyr Leu Arg Arg Leu Lys
1 5 10 15

Gln Glu Leu Met Ser Met Lys Glu Val Gly Asp Gly Leu Gln Asp Gln
20 25 30

Met Asn Cys Met Met Gly Ala Leu Gln Glu Leu Lys Leu Leu Gln Val
35 40 45

Gln Thr Ala Leu Glu Gln Leu Glu Ile Ser Gly Gly Gly Pro Val Pro
50 55 60

Gly Ser Pro Glu Gly Pro Arg Thr Gln Cys Glu His Pro Cys Trp Glu
65 70 75 80

Gly Gly Arg Gly Pro Ala Arg Pro Thr Val Cys Ser Pro Ser Ser Gln
85 90 95

Pro Ser Leu Gly Ser Ser Thr Lys Phe Pro Ser His Arg Ser Val Cys
100 105 110

Gly Arg Asp Leu Ala Pro Leu Pro Arg Thr Gln Pro His Gln Ser Cys
115 120 125

Ala Gln Gln Gly Pro Glu Arg Val Glu Pro Asp Asp Trp Thr Ser Thr
130 135 140

Leu Met Ser Arg Gly Arg Asn Arg Gln Pro Leu Val Leu Gly Asp Asn
145 150 155 160

Val Phe Ala Asp Leu Val Gly Asn Trp Leu Asp Leu Pro Glu Leu Glu
165 170 175

Lys Gly Gly Glu Lys Gly Glu Thr Gly Gly Ala Arg Glu Pro Lys Gly
180 185 190

Glu Lys Gly Gln Pro Gln Glu Leu Gly Arg Arg Phe Ala Leu Thr Ala
195 200 205

Asn Ile Phe Lys Lys Phe Leu Arg Ser Val Arg Pro Asp Arg Asp Arg
210 215 220

Leu Leu Lys Glu Lys Pro Gly Trp Val Thr Pro Met Val Pro Glu Ser
225 230 235 240

Arg Thr Gly Arg Ser Gln Lys Val Lys Lys Arg Ser Leu Ser Lys Gly
245 250 255

Ser Gly His Phe Pro Phe Pro Gly Thr Gly Glu His Arg Arg Gly Glu
260 265 270

Asn Pro Pro Thr Ser Cys Pro Lys Ala Leu Glu His Ser Pro Ser Gly
275 280 285

Phe Asp Ile Asn Thr Ala Val Trp Val
290 295

<210> 47
<211> 1919
<212> DNA
<213> Homo sapiens

<400> 47
ggagctcccc gcatcctgca gtgcattgcc caggagaaaag tgatccctgc acttgcctgt 60
ctgggacaag ggaaggggcc aaacaaaaca cccgtggctg ccatctgcct gaccagcttg 120
gtgaccatgg cctttgtttt tgtgggtcaa gtgaacgttc tggcccccatt cgtcaccatc 180
aacttcatgc tgacatacgt tgcagtggac tactcttact tctccctgtc catgtgttcc 240
tgcagcctga ccccggtgcc tgagccggtg ctcagggagg gcgcagaagg cctccactgc 300
tctgagcacc tgctcttaga gaaagctccc agttacggct ctgagggacc tgcccaaaga 360
gtcttggagg gcacgctact ggaattcacc aaggacatgg atcagctcct ccagctaacc 420
aggaagcttg agagtagcca gcccaggcaa ggagagggtg acaggacccc agaaagtcag 480
aagaggaaaa gcaagaaggc caccaagcag accctacaag atagcttcct cttggacctc 540
aaatcccctc cttctttccc tgtcgagatc tctgacaggt tgcccgtgc ctctggggag 600
gggcaggagt cctgctggaa caagcagact tccaagagcg aagggactca gcctgaggga 660
acatatggag agcaacttgt tctgagctg tgcaaccaat cagagtccag tggagaagat 720
ttcttctga agtccaggct ccaagaacaa gatgtctgga gaagatccac ttctttctat 780
accacatgt gcaaccctg ggtctccctg ttgggggctg ttgggtccct tctcatcatg 840
tttgtgatac agtgggtgta taccctgggt aacatgggtg ttgctgccat cgtgtatttc 900

tacattggcc gggccagtcc agggcttcac ctgggatcag cctccaactt cagctttttc 960
 cggatggatga ggtctctctt gctcccctcc tgcaggagct tgcagtcccc ccaggagcag 1020
 atcatcttgg cgccgtccct ggctaagggt gacatggaga tgactcagct caccaggag 1080
 aatgcagact tcgccactcg ggatcgctac caccactcct ccctcgtgaa ccgggagcag 1140
 ctgatgcctc actactagat gcagtgcctg gaccttcctc ttttggagct gtcccatgta 1200
 cagtggaccc aagcccagga cttcgtgga gctgcttctc caacctgaga aactcaagac 1260
 ccatcctccc gctgtcactt tggacaatgg aaatctacat tttcttttcc cttttttttt 1320
 ttttttgaga cagagtctcg cttgtcacc caggctggag tccagtggca caatcttggc 1380
 tcactgcaac ctctgcttcc cgagttcaag caattctcct gcctcagcct cctgagtagc 1440
 tgggattata ggcattgcacc accacacca gctatttttt gtatttttac tggagacagg 1500
 gtttcacat gttggccagg ctgggtctga actcctgacc tcgtgatcca ccggtctcag 1560
 cctcccaaag tactgggatt acaggcgtga gccaccatgc ctggccagaa atctatgttt 1620
 tcttagaaca tgtggaagaa ggaaaaagac aaaaaaggaa gtctggattc tgaggaccac 1680
 gtctcaccca ggggtgacatc aggaatggtg ctagcctctg caacacgaca ccagctctga 1740
 agagctctat acaggtacta agactagcag gggacaccaa gactctgcac aaccagattg 1800
 cttgtgcaga gggccacaat aagtgtatgt tttatatatt attgtattat ttattcaaaa 1860
 ataaataata cactcacatg tttccacacc caaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1919

<210> 48
 <211> 308
 <212> PRT
 <213> Homo sapiens

<400> 48

Met Cys Ser Cys Ser Leu Thr Pro Val Pro Glu Pro Val Leu Arg Glu
1 5 10 15

Gly Ala Glu Gly Leu His Cys Ser Glu His Leu Leu Leu Glu Lys Ala
20 25 30

Pro Ser Tyr Gly Ser Glu Gly Pro Ala Gln Arg Val Leu Glu Gly Thr
35 40 45

Leu Leu Glu Phe Thr Lys Asp Met Asp Gln Leu Leu Gln Leu Thr Arg
50 55 60

Lys Leu Glu Ser Ser Gln Pro Arg Gln Gly Glu Gly Asn Arg Thr Pro
65 70 75 80

Glu Ser Gln Lys Arg Lys Ser Lys Lys Ala Thr Lys Gln Thr Leu Gln
85 90 95

Asp Ser Phe Leu Leu Asp Leu Lys Ser Pro Pro Ser Phe Pro Val Glu
100 105 110

Ile Ser Asp Arg Leu Pro Ala Ala Ser Trp Glu Gly Gln Glu Ser Cys
115 120 125

Trp Asn Lys Gln Thr Ser Lys Ser Glu Gly Thr Gln Pro Glu Gly Thr
130 135 140

Tyr Gly Glu Gln Leu Val Pro Glu Leu Cys Asn Gln Ser Glu Ser Ser
145 150 155 160

Gly Glu Asp Phe Phe Leu Lys Ser Arg Leu Gln Glu Gln Asp Val Trp
165 170 175

Arg Arg Ser Thr Ser Phe Tyr Thr His Met Cys Asn Pro Trp Val Ser
180 185 190

Leu Leu Gly Ala Val Gly Ser Leu Leu Ile Met Phe Val Ile Gln Trp
195 200 205

Val Tyr Thr Leu Val Asn Met Gly Val Ala Ala Ile Val Tyr Phe Tyr
210 215 220

Ile Gly Arg Ala Ser Pro Gly Leu His Leu Gly Ser Ala Ser Asn Phe
225 230 235 240

Ser Phe Phe Arg Trp Met Arg Ser Leu Leu Leu Pro Ser Cys Arg Ser
245 250 255

Leu Gln Ser Pro Gln Glu Gln Ile Ile Leu Ala Pro Ser Leu Ala Lys
260 265 270

Val Asp Met Glu Met Thr Gln Leu Thr Gln Glu Asn Ala Asp Phe Ala
275 280 285

Thr Arg Asp Arg Tyr His His Ser Ser Leu Val Asn Arg Glu Gln Leu
 290 295 300

Met Pro His Tyr
 305

<210> 49
 <211> 772
 <212> DNA
 <213> Homo sapiens

<400> 49
 tgtcttttagt ttactcagca tcagctacta acatacctga acgaagatct tgttctaaga 60
 cattgtatgt gaagatgata cctgcaaaag acatggctaa agttatgatt gtcagtgttg 120
 caatttgttt tcttacaaaa tcggatggga aatctgttaa gaagagatct gtgagtgaaa 180
 tacagcttat gcataacctg ggaaaacatc tgaactcgat ggagagagta gaatggctgc 240
 gtaagaagct gcaggatgtg cacaattttg ttgcccttgg agctcctcta gctcccagag 300
 atgctggttc ccagaggccc cgaaaaaagg aagacaatgt cttggttgag agccatgaaa 360
 aaagtcttgg agaggcagac aaagctgatg tgaatgtatt aactaaagct aaatcccagt 420
 gaaaatgaaa acagatattg tcagagttct gctctagaca gtgtagggca acaatacatg 480
 ctgctaattc aaagctctat taagatttcc aagtgccaat atttctgata taacaaacta 540
 catgtaatcc atcactagcc atgataactg caattttaat tgattattct gattccactt 600
 ttattcattt gagttatttt aattatcttt tctattgttt attcttttta aagtatgtta 660
 ttgcataatt tataaaagaa taaaattcga cttttaaac tctcttctac cttaaaatgt 720
 aaaacaaaaa tgtaatgatc ataagtctaa ataaatgaag tatttctcac tc 772

<210> 50
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 50

Met Ile Pro Ala Lys Asp Met Ala Lys Val Met Ile Val Met Leu Ala
 1 5 10 15

Ile Cys Phe Leu Thr Lys Ser Asp Gly Lys Ser Val Lys Lys Arg Ser
 20 25 30

Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn Ser
35 40 45

Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His Asn
50 55 60

Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp Ala Gly Ser Gln
65 70 75 80

Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val Glu Ser His Glu Lys
85 90 95

Ser Leu Gly Glu Ala Asp Lys Ala Asp Val Asn Val Leu Thr Lys Ala
100 105 110

Lys Ser Gln
115

<210> 51
<211> 1742
<212> DNA
<213> Homo sapiens

<400> 51
gttagagaga agcgagctgc tgtctgacca gcagcttggg attggtggaa ggaagcaggc 60
caggccctgt gaggagtcaa ggttctgagc agacaggcca accggaggac aggattccct 120
ggaggccaca gaggagcacc aaggagaaga tctgcctgtg ggtccccatt gccagcttt 180
tgcttgcaact cttgcctgct gccctgagca gagtcatcat gtcttctgag cagaagagtc 240
agcactgcaa gcctgaggaa ggcgttgagg cccaagaaga ggccctgggc ctggtgggtg 300
cacaggctcc tactactgag gaggcaggagg ctgctgtctc ctctctctct cctctggtcc 360
ctggcaccct ggaggaagtg cctgctgctg agtcagcagg tcctccccag agtcctcagg 420
gagcctctgc cttaccact accatcagct tcaactgtg gaggcaacct aatgagggtt 480
ccagcagcca agaagaggag gggccaagca cctcgctga cgcagagtc ttgttccgag 540
aagcactcag taacaagggt gatgagttgg ctcatcttct gctccgcaag tatcgagcca 600
aggagctggt cacaaggca gaaatgctgg agagagtcac caaaaattac aagcgtgct 660
ttcctgtgat cttcggcaaa gcctccgagt cctgaagat gatctttggc attgacgtga 720
aggaagtga cccaccagc aacacctaca ccctgtcac ctgcctgggc ctttctatg 780

```

atggcctgct gggtaataat cagatctttc ccaagacagg ccttctgata atcgctctgg      840
gcacaattgc aatggagggc gacagcgctt ctgaggagga aatctgggag gagctgggtg      900
tgatgggggt gtatgatggg agggagcaca ctgtctatgg ggagcccagg aaactgctca      960
cccaagattg ggtgcaggaa aactacctgg agtaccggca ggtaccgggc agtaatcctg     1020
cgcgctatga gttcctgtgg ggtccaaggg ctctggctga aaccagctat gtgaaagtcc     1080
tggagcatgt ggtcagggc aatgcaagag ttgcattgct ctacccatcc ctgcgtgaag     1140
cagctttgtt agaggaggaa gagggagtct gagcatgagt tgcagccagg gctgtgggga     1200
aggggcaggg ctgggccagt gcatctaaca gccctgtgca gcagcttccc ttgcctcgtg     1260
taacatgagg ccattcttc actctgtttg aagaaaatag tcagtgttct tagtagtggg     1320
tttctatttt gttggatgac ttggagattt atctctgttt ctttttacia ttgttgaaat     1380
gttcctttta atggatggtt gaattaactt cagcatccaa gtttatgaat cgtagttaac     1440
gtatattgct gttaatatag tttaggagta agagtcttgt tttttattca gattgggaaa     1500
tccgttctat tttgtgaatt tgggacataa taacagcagt ggagtaagta tttagaagtg     1560
tgaattcacc gtgaaatagg tgagataaat taaaagatac ttaattcccg ccttatgcct     1620
cagtctattc tgtaaaattt aaaaaatata tatgcatacc tggatttcct tggcttcgtg     1680
aatgtaagag aaattaaatc tgaataaata attctttctg ttaaaaaaaaa aaaaaaaaaa     1740
aa                                                                                   1742

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<210> 52
 <211> 317
 <212> PRT
 <213> Homo sapiens

<400> 52

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Met Ser Ser Glu Gln Lys Ser Gln His Cys Lys Pro Glu Glu Gly Val
1           5           10           15

```

```

Glu Ala Gln Glu Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Thr
          20           25           30

```

```

Thr Glu Glu Gln Glu Ala Ala Val Ser Ser Ser Ser Pro Leu Val Pro
      35           40           45

```

```

Gly Thr Leu Glu Glu Val Pro Ala Ala Glu Ser Ala Gly Pro Pro Gln
50           55           60

```

Ser Pro Gln Gly Ala Ser Ala Leu Pro Thr Thr Ile Ser Phe Thr Cys
 65 70 75 80

Trp Arg Gln Pro Asn Glu Gly Ser Ser Ser Gln Glu Glu Gly Pro
 85 90 95

Ser Thr Ser Pro Asp Ala Glu Ser Leu Phe Arg Glu Ala Leu Ser Asn
 100 105 110

Lys Val Asp Glu Leu Ala His Phe Leu Leu Arg Lys Tyr Arg Ala Lys
 115 120 125

Glu Leu Val Thr Lys Ala Glu Met Leu Glu Arg Val Ile Lys Asn Tyr
 130 135 140

Lys Arg Cys Phe Pro Val Ile Phe Gly Lys Ala Ser Glu Ser Leu Lys
 145 150 155 160

Met Ile Phe Gly Ile Asp Val Lys Glu Val Asp Pro Thr Ser Asn Thr
 165 170 175

Tyr Thr Leu Val Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly
 180 185 190

Asn Asn Gln Ile Phe Pro Lys Thr Gly Leu Leu Ile Ile Val Leu Gly
 195 200 205

Thr Ile Ala Met Glu Gly Asp Ser Ala Ser Glu Glu Glu Ile Trp Glu
 210 215 220

Glu Leu Gly Val Met Gly Val Tyr Asp Gly Arg Glu His Thr Val Tyr
 225 230 235 240

Gly Glu Pro Arg Lys Leu Leu Thr Gln Asp Trp Val Gln Glu Asn Tyr
 245 250 255

Leu Glu Tyr Arg Gln Val Pro Gly Ser Asn Pro Ala Arg Tyr Glu Phe
 260 265 270

Leu Trp Gly Pro Arg Ala Leu Ala Glu Thr Ser Tyr Val Lys Val Leu
 275 280 285

Glu His Val Val Arg Val Asn Ala Arg Val Arg Ile Ala Tyr Pro Ser
 290 295 300

Leu Arg Glu Ala Ala Leu Leu Glu Glu Glu Glu Gly Val
 305 310 315

<210> 53
 <211> 1833
 <212> DNA
 <213> Homo sapiens

<400> 53
 ggcacgaggc tgggggtcag agagaagga gaggcctcct tctgaggggc ggcttgatac 60
 cgggtggagga gctccaggaa gcaggcaggc cttgggtctga gacagtgtcc tcagggtcgca 120
 gagcagagga gacccaggca gtgtcagcag tgaaggttct cgggacaggc taaccaggag 180
 gacaggagcc ccaagaggcc ccagagcagc actgacgaag acctgcctgt ggggtctccat 240
 cgcccagctc ctgcccacgc tcttgactgc tgccctgacc agagtcataca tgtctctcga 300
 gcagaggagt ccgcactgca agcctgatga agaccttgaa gccaaggag aggacttggg 360
 cctgatgggt gcacaggaac ccacaggcga ggaggaggag actacctcct cctctgacag 420
 caaggaggag gaggtgtctg ctgctgggtc atcaagtcct cccagagtc ctcaggagg 480
 cgcttctctc tccatttccg tctactacac tttatggagc caattcgatg agggctccag 540
 cagtcaagaa gaggaagagc caagctctc ggtcgacca gctcagctgg agttcatgtt 600
 ccaagaagca ctgaaattga aggtggctga gttgggtcat ttctgtctcc acaaatatcg 660
 agtcaaggag ccggtcacia aggcagaaat gctggagagc gtcataaaaa attacaagcg 720
 ctactttcct gtgatcttcg gcaaagcctc cgagttcatg cagggtgatct ttggcactga 780
 tgtgaaggag gtggaccccg ccggccactc ctacatcctt gtcactgctc ttggcctctc 840
 gtgcgatagc atgctgggtg atggcatag catgcccaag gccgccctcc tgatcattgt 900
 cctgggtgtg atcctaacca aagacaactg cgccctgaa gaggttatct ggggaagcgtt 960
 gagtgtgatg ggggtgtatg ttgggaaggc gcacatgttc tacggggagc ccaggaagct 1020
 gctcacccaa gattgggtgc agaaaaacta cctggagtac cggcaggtgc ccggcagtga 1080
 tctgcgcac tacgagttcc tgtgggggtc caaggccac gctgaaacca gctatgagaa 1140
 ggtcataaat tatttggtca tgctcaatgc aagagagccc atctgctacc catcccttta 1200
 tgaagaggtt ttgggagagg agcaagaggg agtctgagca ccagccgcag ccggggccaa 1260

```

agtttgtggg gtcagggccc catccagcag ctgcctgcc ccatgtgaca tgaggcccat 1320
tcttcgctct gtgtttgaag agagcaatca gtgttctcag tggcagtggg tggaagtgag 1380
cacactgtat gtcactctctg ggttccttgt ctattgggtg atttgagat ttatccttgc 1440
tcccttttgg aattgttcaa atgttctttt aatggtcagt ttaatgaact tcaccatcga 1500
agttaatgaa tgacagtagt cacacatatt gctgtttatg ttatttagga gtaagattct 1560
tgcttttgag tcacatgggg aaatccctgt tattttgtga attgggacaa gataacatag 1620
cagaggaatt aataattttt ttgaaacttg aacttagcag caaataagag ctcataaaga 1680
aatagtgaaa tgaaaatgta gttaattctt gccttatacc tctttctctc tcctgtaaaa 1740
ttaaaacata tacatgtata cctggatttg cttggcttct ttgagcatgt aagagaaata 1800
aaaattgaaa gaataaaaaa aaaaaaaaaa aaa 1833

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<210> 54
<211> 315
<212> PRT
<213> Homo sapiens

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```

<400> 54

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```

Met Ser Leu Glu Gln Arg Ser Pro His Cys Lys Pro Asp Glu Asp Leu
1          5          10          15

```

```

Glu Ala Gln Gly Glu Asp Leu Gly Leu Met Gly Ala Gln Glu Pro Thr
          20          25          30

```

```

Gly Glu Glu Glu Glu Thr Thr Ser Ser Ser Asp Ser Lys Glu Glu Glu
          35          40          45

```

```

Val Ser Ala Ala Gly Ser Ser Ser Pro Pro Gln Ser Pro Gln Gly Gly
50          55          60

```

```

Ala Ser Ser Ser Ile Ser Val Tyr Tyr Thr Leu Trp Ser Gln Phe Asp
65          70          75          80

```

```

Glu Gly Ser Ser Ser Gln Glu Glu Glu Glu Pro Ser Ser Ser Val Asp
          85          90          95

```

```

Pro Ala Gln Leu Glu Phe Met Phe Gln Glu Ala Leu Lys Leu Lys Val
          100          105          110

```

Ala Glu Leu Val His Phe Leu Leu His Lys Tyr Arg Val Lys Glu Pro
 115 120 125
 Val Thr Lys Ala Glu Met Leu Glu Ser Val Ile Lys Asn Tyr Lys Arg
 130 135 140
 Tyr Phe Pro Val Ile Phe Gly Lys Ala Ser Glu Phe Met Gln Val Ile
 145 150 155 160
 Phe Gly Thr Asp Val Lys Glu Val Asp Pro Ala Gly His Ser Tyr Ile
 165 170 175
 Leu Val Thr Ala Leu Gly Leu Ser Cys Asp Ser Met Leu Gly Asp Gly
 180 185 190
 His Ser Met Pro Lys Ala Ala Leu Leu Ile Ile Val Leu Gly Val Ile
 195 200 205
 Leu Thr Lys Asp Asn Cys Ala Pro Glu Glu Val Ile Trp Glu Ala Leu
 210 215 220
 Ser Val Met Gly Val Tyr Val Gly Lys Glu His Met Phe Tyr Gly Glu
 225 230 235 240
 Pro Arg Lys Leu Leu Thr Gln Asp Trp Val Gln Glu Asn Tyr Leu Glu
 245 250 255
 Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala His Tyr Glu Phe Leu Trp
 260 265 270
 Gly Ser Lys Ala His Ala Glu Thr Ser Tyr Glu Lys Val Ile Asn Tyr
 275 280 285
 Leu Val Met Leu Asn Ala Arg Glu Pro Ile Cys Tyr Pro Ser Leu Tyr
 290 295 300
 Glu Glu Val Leu Gly Glu Glu Gln Glu Gly Val
 305 310 315

<210> 55
 <211> 503
 <212> DNA
 <213> Homo sapiens

```

<400> 55
gacagcggct tccttgatcc ttgccacccg cgactgaaca ccgacagcag cagcctcacc      60
atgaagttgc tgatggtcct catgctggcg gccctctccc agcactgcta cgcaggctct      120
ggctgcccct tattggagaa tgtgatttcc aagacaatca atccacaagt gtctaagact      180
gaatacaaag aacttcttca agagttcata gacgacaatg cactacaaa tgccatagat      240
gaattgaagg aatgttttct taaccaaacy gatgaaactc tgagcaatgt tgagggtgtt      300
atgcaattaa tatatgacag cagtctttgt gatatttttt aactttctgc aagacctttg      360
gctcacagaa ctgcagggtg tggtagagaaa ccaactacgg attgctgcaa accacacctt      420
ctctttctta tgtcttttta ctacaaacta caagacaatt gttgaaacct gctatacatg      480
tttattttta taaattgatg gca                                          503

```

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<210> 56
<211> 93
<212> PRT
<213> Homo sapiens

```

```

<400> 56

```

```

Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Ser Gln His Cys
1           5           10           15

```

```

Tyr Ala Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr
20           25           30

```

```

Ile Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu
35           40           45

```

```

Phe Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu
50           55           60

```

```

Cys Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe
65           70           75           80

```

```

Met Gln Leu Ile Tyr Asp Ser Ser Leu Cys Asp Leu Phe
85           90

```

```

<210> 57
<211> 786
<212> DNA
<213> Homo sapiens

```

<400> 57
 atggattggg ggacgctgca cactttcatc ggggggtgtca acaaactc caccagcatc 60
 gggaaggtgt ggatcacagt catctttatt ttccgagtca tgatcctagt ggtggctgcc 120
 caggaagtgt ggggtgacga gcaagaggac ttctgtctgca acacactgca accgggatgc 180
 aaaaatgtgt gctatgacca ctttttcccg gtgtcccaca tccggctgtg ggcctccag 240
 ctgatcttcg tctccacccc agcgtgctg gtggccatgc atgtggccta ctacaggcac 300
 gaaaccactc gcaagttcag gcgaggagag aagaggaatg atttcaaaga catagaggac 360
 attaaaaagc acaaggttcg gatagagggg tcgctgtggt ggacgtacac cagcagcatc 420
 tttttccgaa tcatctttga agcagccttt atgtatgtgt tttacttcct ttacaatggg 480
 taccacctgc cctgggtgtt gaaatgtggg attgaccctt gcccacact tgttgactgc 540
 tttatttcta ggccaacaga gaagaccgtg tttaccattt ttatgatttc tgcgtctgtg 600
 atttgcacgc tgcttaacgt ggcagagttg tgctacctgc tgctgaaagt gtgttttagg 660
 agatcaaaga gagcacagac gcaaaaaaat caccccaatc atgccctaaa ggagagtaag 720
 cagaatgaaa tgaatgagct gatttcagat agtgggtcaaa atgcaatcac aggtttccca 780
 agctaa 786

<210> 58
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 58

Met Asp Trp Gly Thr Leu His Thr Phe Ile Gly Gly Val Asn Lys His
 1 5 10 15

Ser Thr Ser Ile Gly Lys Val Trp Ile Thr Val Ile Phe Ile Phe Arg
 20 25 30

Val Met Ile Leu Val Val Ala Ala Gln Glu Val Trp Gly Asp Glu Gln
 35 40 45

Glu Asp Phe Val Cys Asn Thr Leu Gln Pro Gly Cys Lys Asn Val Cys
 50 55 60

Tyr Asp His Phe Phe Pro Val Ser His Ile Arg Leu Trp Ala Leu Gln
 65 70 75 80

Leu Ile Phe Val Ser Thr Pro Ala Leu Leu Val Ala Met His Val Ala
85 90 95

Tyr Tyr Arg His Glu Thr Thr Arg Lys Phe Arg Arg Gly Glu Lys Arg
100 105 110

Asn Asp Phe Lys Asp Ile Glu Asp Ile Lys Lys His Lys Val Arg Ile
115 120 125

Glu Gly Ser Leu Trp Trp Thr Tyr Thr Ser Ser Ile Phe Phe Arg Ile
130 135 140

Ile Phe Glu Ala Ala Phe Met Tyr Val Phe Tyr Phe Leu Tyr Asn Gly
145 150 155 160

Tyr His Leu Pro Trp Val Leu Lys Cys Gly Ile Asp Pro Cys Pro Asn
165 170 175

Leu Val Asp Cys Phe Ile Ser Arg Pro Thr Glu Lys Thr Val Phe Thr
180 185 190

Ile Phe Met Ile Ser Ala Ser Val Ile Cys Met Leu Leu Asn Val Ala
195 200 205

Glu Leu Cys Tyr Leu Leu Leu Lys Val Cys Phe Arg Arg Ser Lys Arg
210 215 220

Ala Gln Thr Gln Lys Asn His Pro Asn His Ala Leu Lys Glu Ser Lys
225 230 235 240

Gln Asn Glu Met Asn Glu Leu Ile Ser Asp Ser Gly Gln Asn Ala Ile
245 250 255

Thr Gly Phe Pro Ser
260

<210> 59

<211> 1064

<212> DNA

<213> Homo sapiens

<400> 59

attagaattt atcatcaggg aagatatctt ttatgttgag cagctgctat ctgatcttga

60

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cagactgtcc tcttagagga ctgttgaagt ccattctagt cattttgtaa cttcataact 120
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tagtattttc tagtaaatta gttttaatta ttggcagtct gttgggcacc atttgggaaa 600
gaaataaatt ggtctcagt tagcagactt gtagccaaaa actttgaatt aaaaataagt 660
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<210> 60
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 60

Met Val Ser Ala Gly Val Ser Ile Pro Thr Pro Pro Ile Lys Phe Val
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Ile Ser Pro Lys Phe Ser Thr Arg Gly Ser Ala Pro Pro Trp Ala Pro
 20 25 30

Pro Pro Ala Thr Asn Gly Thr Pro Pro Pro Leu Leu Ser Leu Ile Pro
 35 40 45

Pro Pro Phe Pro Pro Ser Ser Ser Pro Pro Pro Phe Pro Pro Val Ser
 50 55 60

Ile Ser Arg Leu Thr Pro Leu Ser Pro Tyr Ser Thr Asn His Pro Pro
65 70 75 80

Leu Pro Pro Leu Tyr Arg Pro Pro Pro Pro Ile Tyr Ile Asn Pro Thr
85 90 95

Ala Ser Leu Ser Phe Pro Pro Leu Phe Ser Pro Thr Pro Ser Tyr Pro
100 105 110

<210> 61

<211> 2511

<212> DNA

<213> Homo sapiens

<400> 61

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cccggcccc cggcccccc agggccgccc ggcaagcccc gccaggacgg cattgacgga      180
gaagctggtc ctccaggtct gcctgggccc ccgggaccaa agggggcccc aggaaagccg      240
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cccgagtg cggggccaag cggagagccg ggcctgccgg gcaaggacgg ccagaatggc      960
gtgccaggac tcgatggcca gaaggagag gctggctgca acggtgctcc gggagagaag     1020
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cggggcagag ctggggagct gggtgaggcc ggccccctct gagagccagg cgtccctgga     1140

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<210> 62
 <211> 684
 <212> PRT
 <213> Homo sapiens

<400> 62

Met Ala Gly Pro Arg Ala Cys Ala Pro Leu Leu Leu Leu Leu Leu

1

5

10

15

Gly Glu Leu Leu Ala Ala Ala Gly Ala Gln Arg Val Gly Leu Pro Gly
 20 25 30

Pro Pro Gly Pro Pro Gly Pro Pro Gly Lys Pro Gly Gln Asp Gly Ile
 35 40 45

Asp Gly Glu Ala Gly Pro Pro Gly Leu Pro Gly Pro Pro Gly Pro Lys
 50 55 60

Gly Ala Pro Gly Lys Pro Gly Lys Pro Gly Glu Ala Gly Leu Pro Gly
 65 70 75 80

Leu Pro Gly Val Asp Gly Leu Thr Gly Arg Asp Gly Pro Pro Gly Pro
 85 90 95

Lys Gly Ala Pro Gly Glu Arg Gly Ser Leu Gly Pro Pro Gly Pro Pro
 100 105 110

Gly Leu Gly Gly Lys Gly Leu Pro Gly Pro Pro Gly Glu Ala Gly Val
 115 120 125

Ser Gly Pro Pro Gly Gly Ile Gly Leu Arg Gly Pro Pro Gly Pro Pro
 130 135 140

Gly Leu Pro Gly Leu Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
 145 150 155 160

His Pro Gly Val Leu Pro Glu Gly Ala Thr Asp Leu Gln Cys Pro Ser
 165 170 175

Ile Cys Pro Pro Gly Pro Pro Gly Pro Pro Gly Met Pro Gly Phe Lys
 180 185 190

Gly Pro Thr Gly Tyr Lys Gly Glu Gln Gly Glu Val Gly Lys Asp Gly
 195 200 205

Glu Lys Gly Asp Pro Gly Pro Pro Gly Pro Ala Gly Leu Pro Gly Ser
 210 215 220

Val Gly Leu Gln Gly Pro Arg Gly Leu Arg Gly Leu Pro Gly Pro Leu
 225 230 235 240

Gly Pro Pro Gly Asp Arg Gly Pro Ile Gly Phe Arg Gly Pro Pro Gly
 245 250 255
 Ile Pro Gly Ala Pro Gly Lys Ala Gly Asp Arg Gly Glu Arg Gly Pro
 260 265 270
 Glu Gly Phe Arg Gly Pro Lys Gly Asp Leu Gly Arg Pro Gly Pro Lys
 275 280 285
 Gly Thr Pro Gly Val Ala Gly Pro Ser Gly Glu Pro Gly Met Pro Gly
 290 295 300
 Lys Asp Gly Gln Asn Gly Val Pro Gly Leu Asp Gly Gln Lys Gly Glu
 305 310 315 320
 Ala Gly Arg Asn Gly Ala Pro Gly Glu Lys Gly Pro Asn Gly Leu Pro
 325 330 335
 Gly Leu Pro Gly Arg Ala Gly Ser Lys Gly Glu Lys Gly Glu Arg Gly
 340 345 350
 Arg Ala Gly Glu Leu Gly Glu Ala Gly Pro Ser Gly Glu Pro Gly Val
 355 360 365
 Pro Gly Asp Ala Gly Met Pro Gly Glu Arg Gly Glu Ala Gly His Arg
 370 375 380
 Gly Ser Ala Gly Ala Leu Gly Pro Gln Gly Pro Pro Gly Ala Pro Gly
 385 390 395 400
 Val Arg Gly Phe Gln Gly Gln Lys Gly Ser Met Gly Asp Pro Gly Leu
 405 410 415
 Pro Gly Pro Gln Gly Leu Arg Gly Asp Val Gly Asp Arg Gly Pro Gly
 420 425 430
 Gly Ala Ala Gly Pro Lys Gly Asp Gln Gly Ile Ala Gly Ser Asp Gly
 435 440 445
 Leu Pro Gly Asp Lys Gly Glu Leu Gly Pro Ser Gly Leu Val Gly Pro
 450 455 460

Lys Gly Glu Ser Gly Ser Arg Gly Glu Leu Gly Pro Lys Gly Thr Gln
 465 470 475 480
 Gly Pro Asn Gly Thr Ser Gly Val Gln Gly Val Pro Gly Pro Pro Gly
 485 490 495
 Pro Leu Gly Leu Gln Gly Val Pro Gly Val Pro Gly Ile Thr Gly Lys
 500 505 510
 Pro Gly Val Pro Gly Lys Glu Ala Ser Glu Gln Arg Ile Arg Glu Leu
 515 520 525
 Cys Gly Gly Met Ile Ser Glu Gln Ile Ala Gln Leu Ala Ala His Leu
 530 535 540
 Arg Lys Pro Leu Ala Pro Gly Ser Ile Gly Arg Pro Gly Pro Ala Gly
 545 550 555 560
 Pro Pro Gly Pro Pro Gly Pro Pro Gly Ser Ile Gly His Pro Gly Ala
 565 570 575
 Arg Gly Pro Pro Gly Tyr Arg Gly Pro Thr Gly Glu Leu Gly Asp Pro
 580 585 590
 Gly Pro Arg Gly Asn Gln Gly Asp Arg Gly Asp Lys Gly Ala Ala Gly
 595 600 605
 Ala Gly Leu Asp Gly Pro Glu Gly Asp Gln Gly Pro Gln Gly Pro Gln
 610 615 620
 Gly Val Pro Gly Thr Ser Lys Asp Gly Gln Asp Gly Ala Pro Gly Glu
 625 630 635 640
 Pro Gly Pro Pro Gly Asp Pro Gly Leu Pro Gly Ala Ile Gly Ala Gln
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<210> 63
 <211> 1441
 <212> DNA
 <213> Homo sapiens

<400> 63
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 agaaggcacc aacctcaacg cgcccaacag cctgggtgtc agcgccctgt gtgccatctg 180
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 gtacatccca gctttctgcg agctccccct ggacgaccag gtggccctgc tcagagccca 660
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 c 1441

<210> 64
 <211> 465
 <212> PRT
 <213> Homo sapiens

<400> 64

Met Asp Met Ala Asp Tyr Ser Ala Ala Leu Asp Pro Ala Tyr Thr Thr
 1 5 10 15

Leu Glu Phe Glu Asn Val Gln Val Leu Thr Met Gly Asn Asp Thr Ser
 20 25 30

Pro Ser Glu Gly Thr Asn Leu Asn Ala Pro Asn Ser Leu Gly Val Ser
 35 40 45

Ala Leu Cys Ala Ile Cys Gly Asp Arg Ala Thr Gly Lys His Tyr Gly
 50 55 60

Ala Ser Ser Cys Asp Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Arg
 65 70 75 80

Lys Asn His Met Tyr Ser Cys Arg Phe Ser Arg Gln Cys Val Val Asp
 85 90 95

Lys Asp Lys Arg Asn Gln Cys Arg Tyr Cys Arg Leu Lys Lys Cys Phe
 100 105 110

Arg Ala Gly Met Lys Lys Glu Ala Val Gln Asn Glu Arg Asp Arg Ile
 115 120 125

Ser Thr Arg Arg Ser Ser Tyr Glu Asp Ser Ser Leu Pro Ser Ile Asn
 130 135 140

Ala Leu Leu Gln Ala Glu Val Leu Ser Arg Gln Ile Thr Ser Pro Val
 145 150 155 160

Ser Gly Ile Asn Gly Asp Ile Arg Ala Lys Lys Ile Ala Ser Ile Ala
 165 170 175

Asp Val Cys Glu Ser Met Lys Glu Gln Leu Leu Val Leu Val Glu Trp
 180 185 190

Ala Lys Tyr Ile Pro Ala Phe Cys Glu Leu Pro Leu Asp Asp Gln Val

195	200	205
Ala Leu Leu Arg Ala His	Ala Gly Glu His Leu	Leu Leu Gly Ala Thr
210	215	220
Lys Arg Ser Met Val Phe	Lys Asp Val Leu	Leu Gly Asn Asp Tyr
225	230	235 240
Ile Val Pro Arg His Cys	Pro Glu Leu Ala	Glu Met Ser Arg Val Ser
245	250	255
Ile Arg Ile Leu Asp Glu	Leu Val Leu Pro	Phe Gln Glu Leu Gln Ile
260	265	270
Asp Asp Asn Glu Tyr Ala	Tyr Leu Lys Ala	Ile Ile Phe Phe Asp Pro
275	280	285
Asp Ala Lys Gly Leu Ser	Asp Pro Gly Lys	Ile Lys Arg Leu Arg Ser
290	295	300
Gln Val Gln Val Ser Leu	Glu Asp Tyr Ile	Asn Asp Arg Gln Tyr Asp
305	310	315 320
Ser Arg Gly Arg Phe Gly	Glu Leu Leu Leu	Leu Leu Pro Thr Leu Gln
325	330	335
Ser Ile Thr Trp Gln Met	Ile Glu Gln Ile	Gln Phe Ile Lys Leu Phe
340	345	350
Gly Met Ala Lys Ile Asp	Asn Leu Leu Gln	Glu Met Leu Leu Gly Gly
355	360	365
Ser Pro Ser Asp Ala Pro	His Ala His His	Pro Leu His Pro His Leu
370	375	380
Met Gln Glu His Met Gly	Thr Asn Val Ile	Val Ala Asn Thr Met Pro
385	390	395 400
Thr His Leu Ser Asn Gly	Gln Met Cys Glu	Trp Pro Arg Pro Arg Gly
405	410	415
Gln Ala Ala Thr Pro Glu	Thr Pro Gln Pro	Ser Pro Pro Gly Ala Ser

420

425

430

Gly Ser Glu Pro Tyr Lys Leu Leu Pro Gly Ala Val Ala Thr Ile Val
 435 440 445

Lys Pro Leu Ser Ala Ile Pro Gln Pro Thr Ile Thr Lys Gln Glu Val
 450 455 460

Ile
 465

<210> 65
 <211> 1323
 <212> DNA
 <213> Homo sapiens

<400> 65
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 ctgcccacac ccatccgctt gcgcattgtg gagctggcgc agctgggcat cggaccctgt 120
 gacatcagtc ggcagctccg cgtatccac ggctgcgtga gcaagatcct ggcgcgctac 180
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 agctccatca gccgcatcct gcgcaacaag atcggcagcc tggcgcgagcc cggaccgtac 420
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<210> 66
 <211> 440
 <212> PRT
 <213> Homo sapiens

<400> 66

Met Glu Gln Thr Tyr Gly Glu Val Asn Gln Leu Gly Gly Val Phe Val
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Asn Gly Arg Pro Leu Pro Asn Ala Ile Arg Leu Arg Ile Val Glu Leu
20 25 30

Ala Gln Leu Gly Ile Arg Pro Cys Asp Ile Ser Arg Gln Leu Arg Val
35 40 45

Ser His Gly Cys Val Ser Lys Ile Leu Ala Arg Tyr Asn Glu Thr Gly
50 55 60

Ser Ile Leu Pro Gly Ala Ile Gly Gly Ser Lys Pro Arg Val Thr Thr
65 70 75 80

Pro Asn Val Val Lys His Ile Arg Asp Tyr Lys Gln Gly Asp Pro Gly
85 90 95

Ile Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu Ala Asp Gly Val Cys
100 105 110

Asp Lys Tyr Asn Val Pro Ser Val Ser Ser Ile Ser Arg Ile Leu Arg
115 120 125

Asn Lys Ile Gly Ser Leu Ala Gln Pro Gly Pro Tyr Glu Ala Ser Lys
130 135 140

Gln Pro Pro Ser Gln Pro Thr Leu Pro Tyr Asn His Ile Tyr Gln Tyr
145 150 155 160

Pro Tyr Pro Ser Pro Val Ser Pro Thr Gly Ala Lys Met Gly Ser His
 165 170 175

Pro Gly Val Pro Gly Thr Ala Gly His Val Ser Ile Pro Arg Ser Trp
 180 185 190

Pro Ser Ala His Ser Val Ser Asn Ile Leu Gly Ile Arg Thr Phe Met
 195 200 205

Glu Gln Thr Gly Ala Leu Ala Gly Ser Glu Gly Thr Ala Tyr Ser Pro
 210 215 220

Lys Met Glu Asp Trp Ala Gly Val Asn Arg Thr Ala Phe Pro Ala Thr
 225 230 235 240

Pro Ala Val Asn Gly Leu Glu Lys Pro Ala Leu Glu Ala Asp Ile Lys
 245 250 255

Tyr Thr Gln Ser Ala Ser Thr Leu Ser Ala Val Gly Gly Phe Leu Pro
 260 265 270

Ala Cys Ala Tyr Pro Ala Ser Asn Gln His Gly Val Tyr Ser Ala Pro
 275 280 285

Gly Gly Gly Tyr Leu Ala Pro Gly Pro Pro Trp Pro Pro Ala Gln Gly
 290 295 300

Pro Pro Leu Ala Pro Pro Gly Ala Gly Val Ala Val His Gly Gly Glu
 305 310 315 320

Leu Ala Ala Ala Met Thr Phe Lys His Pro Ser Arg Glu Gly Ser Leu
 325 330 335

Pro Ala Pro Ala Ala Arg Pro Arg Thr Pro Ser Val Ala Tyr Thr Asp
 340 345 350

Cys Pro Ser Arg Pro Arg Pro Pro Arg Gly Ser Ser Pro Arg Thr Arg
 355 360 365

Ala Arg Arg Glu Arg Gln Ala Asp Pro Gly Ala Gln Val Cys Ala Ala
 370 375 380

Ala Pro Ala Ile Gly Thr Gly Arg Ile Gly Gly Leu Ala Glu Glu Glu
385 390 395 400

Ala Ser Ala Gly Pro Arg Gly Ala Arg Pro Ala Ser Pro Gln Ala Gln
405 410 415

Pro Cys Leu Trp Pro Asp Pro Pro His Phe Leu Tyr Trp Ser Gly Phe
420 425 430

Leu Gly Phe Ser Glu Leu Gly Phe
435 440

<210> 67
<211> 416
<212> DNA
<213> Homo sapiens

<400> 67
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tccctttcta ctttaccttc tcatttcttg aagtctctat tctcattaat ttgttattta 180
gttacagtcc tcttttcagt ttcttcagat ggggatatgc agatgataga ttcttggaat 240
cctttctgca tccctttcac tctggcaggt gaatgatgct tggctggaaa gagacttctt 300
ggttactttc cttttctctt aacaggtata gatatgattc cactgtctga taccagttcca 360
attcttttcc cattgcaaatt aacttctttc tgtctggaat cttatatatt tttctc 416

<210> 68
<211> 108
<212> PRT
<213> Homo sapiens

<400> 68

Met Tyr Ile Thr Arg Leu Ile Val His Ser Ser Ser Ser Leu Ser Thr
1 5 10 15

Leu Pro Ser His Phe Leu Lys Ser Leu Phe Ser Leu Ile Cys Tyr Leu
20 25 30

Val Thr Val Leu Phe Ser Val Ser Ser Asp Gly Asp Met Gln Met Ile
35 40 45

Asp Ser Trp Asn Pro Phe Cys Ile Pro Phe Thr Leu Ala Gly Glu Leu
50 55 60

Ala Gly Lys Arg Leu Leu Gly Tyr Phe Pro Phe Leu Leu Thr Gly Ile
65 70 75 80

Asp Met Ile Pro Leu Ser Asp Thr Ser Pro Ile Leu Phe Pro Leu Gln
85 90 95

Ile Thr Ser Phe Cys Leu Glu Ser Tyr Ile Phe Phe
100 105

<210> 69

<211> 2595

<212> DNA

<213> Homo sapiens

<400> 69

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agcgccaaca gttgcggcgg cgacgaccgc ttcctagtgg gcaggggggt gcagatcggt      180
tcgccccacc accaccacca ccaccacat caccacccc agccggctac ctaccagact      240
tccgggaacc tgggggtgtc ctactccac tcaagttgtg gtccaagcta tggctcacag      300
aacttcagty cgccttacag cccctacgcy ttaaatacagg aagcagacgt aagtgggtgg      360
tacccccagt gcgctccgc tgtttactct ggaaatctct catctccat ggtccagcat      420
caccaccacc accaggggta tgctgggggc gcggtgggct cgcctcaata cattcaccac      480
tcatatggac aggagcacca gagcctggcc ctggctacgt ataataactc cttgtcccct      540
ctccacgcca gccaccaaga agcctgtcgc tccccgcgt cggagacatc ttctccagcg      600
cagacttttg actggatgaa agtcaaaaga aaccctccca aaacagggtca gtcctgctgg      660
ttggtggatg ctccttgatt attctggaag gagctggat gcttaatttc caaggaaatt      720
aataatgatc ttttttttaa aaggcttttg tatcagacta gtgtttagt gcatggagag      780
ggtgcccaga ggtgttgggg caaagaagtc tcagggattg gtgtgttttc aaggatttta      840
tacatttggg aaataggaag tatgtggggg tggttattgt gacggtagt ttctgttaat      900
atcttgaggc tccattaatc accggtctga ccattgtaac ggtttacatc aggttaacac      960
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<210> 70

<211> 330
 <212> PRT
 <213> Homo sapiens
 <400> 70

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 20 25 30

Gln Ser Cys Ala Val Ser Ala Asn Ser Cys Gly Gly Asp Asp Arg Phe
 35 40 45

Leu Val Gly Arg Gly Val Gln Ile Gly Ser Pro His His His His His
 50 55 60

His His His His His Pro Gln Pro Ala Thr Tyr Gln Thr Ser Gly Asn
 65 70 75 80

Leu Gly Val Ser Tyr Ser His Ser Ser Cys Gly Pro Ser Tyr Gly Ser
 85 90 95

Gln Asn Phe Ser Ala Pro Tyr Ser Pro Tyr Ala Leu Asn Gln Glu Ala
 100 105 110

Asp Val Ser Gly Gly Tyr Pro Gln Cys Ala Pro Ala Val Tyr Ser Gly
 115 120 125

Asn Leu Ser Ser Pro Met Val Gln His His His His His Gln Gly Tyr
 130 135 140

Ala Gly Gly Ala Val Gly Ser Pro Gln Tyr Ile His His Ser Tyr Gly
 145 150 155 160

Gln Glu His Gln Ser Leu Ala Leu Ala Thr Tyr Asn Asn Ser Leu Ser
 165 170 175

Pro Leu His Ala Ser His Gln Glu Ala Cys Arg Ser Pro Ala Ser Glu
 180 185 190

Thr Ser Ser Pro Ala Gln Thr Phe Asp Trp Met Lys Val Lys Arg Asn
 195 200 205

Pro Pro Lys Thr Gly Lys Val Gly Glu Tyr Gly Tyr Leu Gly Gln Pro
210 215 220

Asn Ala Val Arg Thr Asn Phe Thr Thr Lys Gln Leu Thr Glu Leu Glu
225 230 235 240

Lys Glu Phe His Phe Asn Lys Tyr Leu Thr Arg Ala Arg Arg Val Glu
245 250 255

Ile Ala Ala Ser Leu Gln Leu Asn Glu Thr Gln Val Lys Ile Trp Phe
260 265 270

Gln Asn Arg Arg Met Lys Gln Lys Lys Arg Glu Lys Glu Gly Leu Leu
275 280 285

Pro Ile Ser Pro Ala Thr Pro Pro Gly Asn Asp Glu Lys Ala Glu Glu
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Ser Ser Glu Lys Ser Ser Ser Ser Pro Cys Val Pro Ser Pro Gly Ser
305 310 315 320

Ser Thr Ser Asp Thr Leu Thr Thr Ser His
325 330

<210> 71
<211> 222
<212> PRT
<213> Homo sapiens

<400> 71

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Thr Cys Ser Ala Arg Ala Tyr Pro Ser Asp His Arg Ile Thr Thr Phe
20 25 30

Gln Ser Cys Ala Val Ser Ala Asn Ser Cys Gly Gly Asp Asp Arg Phe
35 40 45

Leu Val Gly Arg Gly Val Gln Ile Gly Ser Pro His His His His His
50 55 60

His His His His His Pro Gln Pro Ala Thr Tyr Gln Thr Ser Gly Asn
 65 70 75 80
 Leu Gly Val Ser Tyr Ser His Ser Ser Cys Gly Pro Ser Tyr Gly Ser
 85 90 95
 Gln Asn Phe Ser Ala Pro Tyr Ser Pro Tyr Ala Leu Asn Gln Glu Ala
 100 105 110
 Asp Val Ser Gly Gly Tyr Pro Gln Cys Ala Pro Ala Val Tyr Ser Gly
 115 120 125
 Asn Leu Ser Ser Pro Met Val Gln His His His His His Gln Gly Tyr
 130 135 140
 Ala Gly Gly Ala Val Gly Ser Pro Gln Tyr Ile His His Ser Tyr Gly
 145 150 155 160
 Gln Glu His Gln Ser Leu Ala Leu Ala Thr Tyr Asn Asn Ser Leu Ser
 165 170 175
 Pro Leu His Ala Ser His Gln Glu Ala Cys Arg Ser Pro Ala Ser Glu
 180 185 190
 Thr Ser Ser Pro Ala Gln Thr Phe Asp Trp Met Lys Val Lys Arg Asn
 195 200 205
 Pro Pro Lys Thr Gly Gln Ser Cys Trp Leu Val Asp Ala Pro
 210 215 220
 <210> 72
 <211> 132
 <212> PRT
 <213> Homo sapiens
 <400> 72
 Met Asn Ser Phe Leu Glu Tyr Pro Ile Leu Ser Ser Gly Asp Ser Gly
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 Thr Cys Ser Ala Arg Ala Tyr Pro Ser Asp His Arg Ile Thr Thr Phe
 20 25 30
 Gln Ser Cys Ala Val Ser Ala Asn Ser Cys Gly Gly Asp Asp Arg Phe

35

40

45

Leu Val Gly Arg Gly Val Gln Ile Gly Ser Pro His His His His His
50 55 60

His His His His His Pro Gln Pro Ala Thr Tyr Gln Thr Ser Gly Asn
65 70 75 80

Leu Gly Val Ser Tyr Ser His Ser Ser Cys Gly Pro Ser Tyr Gly Ser
85 90 95

Gln Asn Phe Ser Ala Pro Tyr Ser Pro Tyr Ala Leu Asn Gln Glu Ala
100 105 110

Asp Pro Pro Arg Ser Leu Ser Leu Pro Arg Ile Gly Asp Ile Phe Ser
115 120 125

Ser Ala Asp Phe
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<210> 73
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<212> DNA
<213> Homo sapiens

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<400> 73
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gtttgggaaa atttttccag gatgttttca gatgagtttg tgaacaatgg ccctagagta 180
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<210> 74
<211> 52

<212> PRT
 <213> Homo sapiens

<220>
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 <222> (20)..(20)
 <223> X = unknown

<400> 74

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Asn Gly Ala Xaa Cys Cys Leu Met Gln Ser Pro Gln Asn Ile Ser Arg
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Thr Thr Ser Gln Ile Glu Phe Gln Val Pro His Arg Lys Arg Arg Asp
 35 40 45

Gln Ala Pro Pro
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<210> 75
 <211> 2447
 <212> DNA
 <213> Homo sapiens

<400> 75

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2447

<210> 76
 <211> 451
 <212> PRT
 <213> Homo sapiens

<400> 76

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Ala Val Val Gly Thr Gly Leu Asn Val Arg Leu Met Leu Tyr Thr Arg
 35 40 45

Lys Asn Leu Thr Cys Ala Gln Thr Ile Asn Ser Ser Ala Phe Gly Asn
 50 55 60

Leu Asn Val Thr Lys Lys Thr Thr Phe Ile Val His Gly Phe Arg Pro
 65 70 75 80

Thr Gly Ser Pro Pro Val Trp Met Asp Asp Leu Val Lys Gly Leu Leu
 85 90 95

Ser Val Glu Asp Met Asn Val Val Val Val Asp Trp Asn Arg Gly Ala
 100 105 110

Thr Thr Leu Ile Tyr Thr His Ala Ser Ser Lys Thr Arg Lys Val Ala
 115 120 125

Met Val Leu Lys Glu Phe Ile Asp Gln Met Leu Ala Glu Gly Ala Ser
 130 135 140

Leu Asp Asp Ile Tyr Met Ile Gly Val Ser Leu Gly Ala His Ile Ser
 145 150 155 160

Gly Phe Val Gly Glu Met Tyr Asp Gly Trp Leu Gly Arg Ile Thr Gly
 165 170 175

Leu Asp Pro Ala Gly Pro Leu Phe Asn Gly Lys Pro His Gln Asp Arg
 180 185 190

Leu Asp Pro Ser Asp Ala Gln Phe Val Asp Val Ile His Ser Asp Thr
 195 200 205
 Asp Ala Leu Gly Tyr Lys Glu Pro Leu Gly Asn Ile Asp Phe Tyr Pro
 210 215 220
 Asn Gly Gly Leu Asp Gln Pro Gly Cys Pro Lys Thr Ile Leu Gly Gly
 225 230 235 240
 Phe Gln Tyr Phe Lys Cys Asp His Gln Arg Ser Val Tyr Leu Tyr Leu
 245 250 255
 Ser Ser Leu Arg Glu Ser Cys Thr Ile Thr Ala Tyr Pro Cys Asp Ser
 260 265 270
 Tyr Gln Asp Tyr Arg Asn Gly Lys Cys Val Ser Cys Gly Thr Ser Gln
 275 280 285
 Lys Glu Ser Cys Pro Leu Leu Gly Tyr Tyr Ala Asp Asn Trp Lys Asp
 290 295 300
 His Leu Arg Gly Lys Asp Pro Pro Met Thr Lys Ala Phe Phe Asp Thr
 305 310 315 320
 Ala Glu Glu Ser Pro Phe Cys Met Tyr His Tyr Phe Val Asp Ile Ile
 325 330 335
 Thr Trp Asn Lys Asn Val Arg Arg Gly Asp Ile Thr Ile Lys Leu Arg
 340 345 350
 Asp Lys Ala Gly Asn Thr Thr Glu Ser Lys Ile Asn His Glu Pro Thr
 355 360 365
 Thr Phe Gln Lys Tyr His Gln Val Ser Leu Leu Ala Arg Phe Asn Gln
 370 375 380
 Asp Leu Asp Lys Val Ala Ala Ile Ser Leu Met Phe Ser Thr Gly Ser
 385 390 395 400
 Leu Ile Gly Pro Arg Tyr Lys Leu Arg Ile Leu Arg Met Lys Leu Arg
 405 410 415

Ser Leu Ala His Pro Glu Arg Pro Gln Leu Cys Arg Tyr Asp Leu Val
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Leu Gln Leu
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<210> 77

<211> 2482

<212> DNA

<213> Homo sapiens

<400> 77

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<210> 78

<211> 443

<212> PRT

<213> Homo sapiens

<400> 78

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His Tyr Asn Tyr Tyr Ala Thr Leu Leu Thr Leu Leu Ile Ala Val Ile
 35 40 45

Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser Arg Glu Lys Ala
 50 55 60

Leu Gln Thr Thr Thr Asn Tyr Leu Ile Val Ser Leu Ala Val Ala Asp
 65 70 75 80

Leu Leu Val Ala Thr Leu Val Met Pro Trp Val Val Tyr Leu Glu Val
 85 90 95

Val Gly Glu Trp Lys Phe Ser Arg Ile His Cys Asp Ile Phe Val Thr
 100 105 110

Leu Asp Val Met Met Cys Thr Ala Ser Ile Leu Asn Leu Cys Ala Ile
 115 120 125

Ser Ile Asp Arg Tyr Thr Ala Val Ala Met Pro Met Leu Tyr Asn Thr
 130 135 140

Arg Tyr Ser Ser Lys Arg Arg Val Thr Val Met Ile Ser Ile Val Trp
 145 150 155 160

Val Leu Ser Phe Thr Ile Ser Cys Pro Leu Leu Phe Gly Leu Asn Asn
 165 170 175

Ala Asp Gln Asn Glu Cys Ile Ile Ala Asn Pro Ala Phe Val Val Tyr
 180 185 190

Ser Ser Ile Val Ser Phe Tyr Val Pro Phe Ile Val Thr Leu Leu Val
 195 200 205

Tyr Ile Lys Ile Tyr Ile Val Leu Arg Arg Arg Arg Lys Arg Val Asn
 210 215 220

Thr Lys Arg Ser Ser Arg Ala Phe Arg Ala His Leu Arg Ala Pro Leu
 225 230 235 240

Lys Gly Asn Cys Thr His Pro Glu Asp Met Lys Leu Cys Thr Val Ile
245 250 255

Met Lys Ser Asn Gly Ser Phe Pro Val Asn Arg Arg Arg Val Glu Ala
260 265 270

Ala Arg Arg Ala Gln Glu Leu Glu Met Glu Met Leu Ser Ser Thr Ser
275 280 285

Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser His His Gln
290 295 300

Leu Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Thr Pro Asp
305 310 315 320

Ser Pro Ala Lys Pro Glu Lys Asn Gly His Ala Lys Asp His Pro Lys
325 330 335

Ile Ala Lys Ile Phe Glu Ile Gln Thr Met Pro Asn Gly Lys Thr Arg
340 345 350

Thr Ser Leu Lys Thr Met Ser Arg Arg Lys Leu Ser Gln Gln Lys Glu
355 360 365

Lys Lys Ala Thr Gln Met Leu Ala Ile Val Leu Gly Val Phe Ile Ile
370 375 380

Cys Trp Leu Pro Phe Phe Ile Thr His Ile Leu Asn Ile His Cys Asp
385 390 395 400

Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr Trp Leu Gly Tyr
405 410 415

Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile Glu
420 425 430

Phe Arg Lys Ala Phe Leu Lys Ile Leu His Cys
435 440

<210> 79

<211> 659

<212> DNA

<213> Homo sapiens

<400> 79
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 <211> 166
 <212> PRT
 <213> Homo sapiens

<400> 80

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Ser Asp Gly Gly Asp Ser Glu Gln Phe Ile Asp Glu Glu Arg Gln Gly
 35 40 45

Pro Pro Leu Gly Gly Gln Gln Ser Gln Pro Ser Ala Gly Asp Gly Asn
 50 55 60

Gln Asn Asp Gly Pro Gln Gln Gly Pro Pro Gln Gln Gly Gly Gln Gln
 65 70 75 80

Gln Gln Gly Pro Pro Pro Pro Gln Gly Lys Pro Gln Gly Pro Pro Gln
 85 90 95

Gln Gly Gly His Pro Pro Pro Pro Gln Gly Arg Pro Gln Gly Pro Pro

100

105

110

Gln Gln Gly Gly His Pro Arg Pro Pro Arg Gly Arg Pro Gln Gly Pro
 115 120 125

Pro Gln Gln Gly Gly His Gln Gln Gly Pro Pro Pro Pro Pro Gly
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Lys Pro Gln Gly Pro Pro Pro Gln Gly Gly Arg Pro Gln Gly Pro Pro
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Gln Gly Gln Ser Pro Gln
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<210> 81
 <211> 574
 <212> DNA
 <213> Homo sapiens

<400> 81
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 agatggagag tgagaagaat tatgatgagt tcatgaagct ccttgggatc tccagcgatg 180
 taatcgaaaa ggcccacaac ttcaagatcg tcacggaggt gcagcaggat gggcaggact 240
 tcacttggtc ccagcactac tacggggggc acaccatgac caacaagttc actgttggca 300
 aggaaagcaa catacagaca atggggggca agacgttcaa ggccactgtg cagatggagg 360
 gcgggaagct ggtggtgaat ttccccaact atcaccagac ctacagagatc gtgggtgaca 420
 agctggtgga ggtctccacc atcggaggcg tgacctatga gcgctgagc aagagactgg 480
 cctaagcagc caggcccggc ccaggagct acaaaccac caataaaact gatataagga 540
 cagacgctaa aaaaaaagaa aaaaaaaaaa aaaa 574

<210> 82
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 82

Met Ala Phe Thr Gly Lys Phe Glu Met Glu Ser Glu Lys Asn Tyr Asp
 1 5 10 15

Glu Phe Met Lys Leu Leu Gly Ile Ser Ser Asp Val Ile Glu Lys Ala
 20 25 30

His Asn Phe Lys Ile Val Thr Glu Val Gln Gln Asp Gly Gln Asp Phe
 35 40 45

Thr Trp Ser Gln His Tyr Tyr Gly Gly His Thr Met Thr Asn Lys Phe
 50 55 60

Thr Val Gly Lys Glu Ser Asn Ile Gln Thr Met Gly Gly Lys Thr Phe
 65 70 75 80

Lys Ala Thr Val Gln Met Glu Gly Gly Lys Leu Val Val Asn Phe Pro
 85 90 95

Asn Tyr His Gln Thr Ser Glu Ile Val Gly Asp Lys Leu Val Glu Val
 100 105 110

Ser Thr Ile Gly Gly Val Thr Tyr Glu Arg Val Ser Lys Arg Leu Ala
 115 120 125

<210> 83
 <211> 1942
 <212> DNA
 <213> Homo sapiens

<400> 83
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 cgggtgccagc aggcagccct gggctggggg taggggactc cctacaggca cgcagccctg 180
 agacctcaga gggccacccc ttgagggtgg ccaggccccc agtggccaac ctgagtgtctg 240
 cctctgccac cagccctgct ggcccctggt tccgttggcc ccccagatgc ctggctgaga 300
 cacgccagtg gcctcagctg cccacacctc ttcccggccc ctgaagttag cactgcagca 360
 gacagctccc tgggcaccag gcagctaaca gacacagccg ccagcccaaa cagcagcggc 420
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 gacacggtgt cgcggacagg cttggagaag gcggcagcgg gggcagtggg tctcgagaga 540
 cgggactgga gtcccagtcc acccgccacg cccgagcagg gcctgtccgc cttctacctc 600
 tctacttttg acatgctgta ccctgaggac agcagctggg cagccaaggc ccctggggcc 660

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agcagtcggg aggagccacc tgaggagcct gagcagtgcc cggtcattga cagccaagcc 720
ccagcgggca gcctggactt ggtgcccggc gggctgacct tggaggagca ctcgctggag 780
caggtgcagt ccatggtggt gggcgaagtg ctcaaggaca tcgagacggc ctgcaagctg 840
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tggacagagc accaataaccg gctgcccccc atgggcaagg ccttccagga gctggcgggc 960
aaggagctgt gcgccatgtc ggaggagcag ttccgccagc gctcgcccct ggggtgggat 1020
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cctggggcga ttactactg tgctcgcacc agtgaggaga gctggaccga cagcgaggtg 1140
gactcatcat gctccgggca gcccatccac ctgtggcagt tcctcaagga gttgctactc 1200
aagccccaca gctatggccg cttcattagg tggctcaaca aggagaaggg catcttcaaa 1260
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ccagacatct cccagcgcct cgtctaccag ttctgtgcacc ccatctgagt gcctggccca 1440
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agatggggga aaacgggcag tctgtctgct tgctctgacc ttccagagcc caaggtcagg 1560
gaggggcaac caactgcccc agggggatat gggctcctctg gggccttcgg gaccctgggg 1620
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ctgcaccaca cctggcatgg tgcagggaga catctgcacc cctgagttgg gcagccagga 1860
gtgcccccg gaatggataa taaagatact agagaactga aaaaaaaaaa aaaaaaaaaa 1920
aaacaaaaaa aaaaaaaaaa aa 1942

```

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<210> 84
<211> 335
<212> PRT
<213> Homo sapiens

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<400> 84

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Met Gly Ser Ala Ser Pro Gly Leu Ser Ser Val Ser Pro Ser His Leu
1           5           10           15

```


Leu Leu Pro Pro Asp Thr Val Ser Arg Thr Gly Leu Glu Lys Ala Ala
 20 25 30
 Ala Gly Ala Val Gly Leu Glu Arg Arg Asp Trp Ser Pro Ser Pro Pro
 35 40 45
 Ala Thr Pro Glu Gln Gly Leu Ser Ala Phe Tyr Leu Ser Tyr Phe Asp
 50 55 60
 Met Leu Tyr Pro Glu Asp Ser Ser Trp Ala Ala Lys Ala Pro Gly Ala
 65 70 75 80
 Ser Ser Arg Glu Glu Pro Pro Glu Glu Pro Glu Gln Cys Pro Val Ile
 85 90 95
 Asp Ser Gln Ala Pro Ala Gly Ser Leu Asp Leu Val Pro Gly Gly Leu
 100 105 110
 Thr Leu Glu Glu His Ser Leu Glu Gln Val Gln Ser Met Val Val Gly
 115 120 125
 Glu Val Leu Lys Asp Ile Glu Thr Ala Cys Lys Leu Leu Asn Ile Thr
 130 135 140
 Ala Asp Pro Met Asp Trp Ser Pro Ser Asn Val Gln Lys Trp Leu Leu
 145 150 155 160
 Trp Thr Glu His Gln Tyr Arg Leu Pro Pro Met Gly Lys Ala Phe Gln
 165 170 175
 Glu Leu Ala Gly Lys Glu Leu Cys Ala Met Ser Glu Glu Gln Phe Arg
 180 185 190
 Gln Arg Ser Pro Leu Gly Gly Asp Val Leu His Ala His Leu Asp Ile
 195 200 205
 Trp Lys Ser Ala Ala Trp Met Lys Glu Arg Thr Ser Pro Gly Ala Ile
 210 215 220
 His Tyr Cys Ala Ser Thr Ser Glu Glu Ser Trp Thr Asp Ser Glu Val
 225 230 235 240

Asp Ser Ser Cys Ser Gly Gln Pro Ile His Leu Trp Gln Phe Leu Lys
245 250 255

Glu Leu Leu Leu Lys Pro His Ser Tyr Gly Arg Phe Ile Arg Trp Leu
260 265 270

Asn Lys Glu Lys Gly Ile Phe Lys Ile Glu Asp Ser Ala Gln Val Ala
275 280 285

Arg Leu Trp Gly Ile Arg Lys Asn Arg Pro Ala Met Asn Tyr Asp Lys
290 295 300

Leu Ser Arg Ser Ile Arg Gln Tyr Tyr Lys Lys Gly Ile Ile Arg Lys
305 310 315 320

Pro Asp Ile Ser Gln Arg Leu Val Tyr Gln Phe Val His Pro Ile
325 330 335

<210> 85

<211> 1224

<212> DNA

<213> Homo sapiens

<400> 85

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ggagctctcc ccggtctgac agccactcca gaggccatgc ttcgtttctt gccagatttg      60
gctttcagct tcctgttaat tctggctttg ggccaggcag tccaatttca agaatatgtc      120
tttctccaat ttctgggctt agataaggcg ccttcacccc agaagttcca acctgtgcct      180
tatatcttga agaaaatttt ccaggatcgc gaggcagcag cgaccactgg ggtctcccga      240
gacttatgct acgtaaagga gctgggcgtc cgcgggaatg tacttcgctt tctcccagac      300
caaggtttct ttctttaccc aaagaaaatt tccaagctt cctcctgcct gcagaagctc      360
ctctacttta acctgtctgc catcaaagaa agggaacagt tgacattggc ccagctgggc      420
ctggacttgg ggccaattc ttactataac ctgggaccag agctggaact ggctctgttc      480
ctggttcagg agcctcatgt gtggggccag accacccta agccaggtaa aatgtttgtg      540
ttgcggtcag tcccatggcc acaagggtgt gttcacttca acctgctgga tgtagctaag      600
gattggaatg acaacccccg gaaaaatttc gggttattcc tggagatact ggtcaaagaa      660
gatagagact caggggtgaa ttttcagcct gaagacacct gtgccagact aagatgctcc      720
cttcatgctt ccctgctggt ggtgactctc aaccctgata agtgccaccc ttctcggaaa      780

```

```

aggagagcag ccatccctgt cccaagctt tcttgtaaga acctctgcca ccgtcaccag      840
ctattcatta acttccggga cctgggttgg cacaagtgga tcattgcccc caaggggttc      900
atggcaaatt actgccatgg agagtgtccc ttctcaactga ccattctctct caacagctcc      960
aattatgctt tcatgcaagc cctgatgcat gccgttgacc cagagatccc ccaggctgtg     1020
tgtatcccca ccaagctgtc tcccatttcc atgctctacc aggacaataa tgacaatgtc     1080
attctacgac attatgaaga catggtagtgc gatgaatgtg ggtgtgggta ggatgtcaga     1140
aatgggaata gaaggagtgt tcttagggta aatcttttaa taaaactacc tatctgggtt      1200
atgaccactt agatcgaaat gtca                                           1224

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<210> 86
<211> 364
<212> PRT
<213> Homo sapiens

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```

<400> 86

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```

Met Leu Arg Phe Leu Pro Asp Leu Ala Phe Ser Phe Leu Leu Ile Leu
1           5           10           15

```

```

Ala Leu Gly Gln Ala Val Gln Phe Gln Glu Tyr Val Phe Leu Gln Phe
20           25           30

```

```

Leu Gly Leu Asp Lys Ala Pro Ser Pro Gln Lys Phe Gln Pro Val Pro
35           40           45

```

```

Tyr Ile Leu Lys Lys Ile Phe Gln Asp Arg Glu Ala Ala Thr Thr
50           55           60

```

```

Gly Val Ser Arg Asp Leu Cys Tyr Val Lys Glu Leu Gly Val Arg Gly
65           70           75           80

```

```

Asn Val Leu Arg Phe Leu Pro Asp Gln Gly Phe Phe Leu Tyr Pro Lys
85           90           95

```

```

Lys Ile Ser Gln Ala Ser Ser Cys Leu Gln Lys Leu Leu Tyr Phe Asn
100          105          110

```

```

Leu Ser Ala Ile Lys Glu Arg Glu Gln Leu Thr Leu Ala Gln Leu Gly
115          120          125

```

Leu Asp Leu Gly Pro Asn Ser Tyr Tyr Asn Leu Gly Pro Glu Leu Glu
130 135 140

Leu Ala Leu Phe Leu Val Gln Glu Pro His Val Trp Gly Gln Thr Thr
145 150 155 160

Pro Lys Pro Gly Lys Met Phe Val Leu Arg Ser Val Pro Trp Pro Gln
165 170 175

Gly Ala Val His Phe Asn Leu Leu Asp Val Ala Lys Asp Trp Asn Asp
180 185 190

Asn Pro Arg Lys Asn Phe Gly Leu Phe Leu Glu Ile Leu Val Lys Glu
195 200 205

Asp Arg Asp Ser Gly Val Asn Phe Gln Pro Glu Asp Thr Cys Ala Arg
210 215 220

Leu Arg Cys Ser Leu His Ala Ser Leu Leu Val Val Thr Leu Asn Pro
225 230 235 240

Asp Gln Cys His Pro Ser Arg Lys Arg Arg Ala Ala Ile Pro Val Pro
245 250 255

Lys Leu Ser Cys Lys Asn Leu Cys His Arg His Gln Leu Phe Ile Asn
260 265 270

Phe Arg Asp Leu Gly Trp His Lys Trp Ile Ile Ala Pro Lys Gly Phe
275 280 285

Met Ala Asn Tyr Cys His Gly Glu Cys Pro Phe Ser Leu Thr Ile Ser
290 295 300

Leu Asn Ser Ser Asn Tyr Ala Phe Met Gln Ala Leu Met His Ala Val
305 310 315 320

Asp Pro Glu Ile Pro Gln Ala Val Cys Ile Pro Thr Lys Leu Ser Pro
325 330 335

Ile Ser Met Leu Tyr Gln Asp Asn Asn Asp Asn Val Ile Leu Arg His
340 345 350

Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys Gly
355 360

<210> 87
<211> 993
<212> DNA
<213> Homo sapiens

<400> 87
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acgggcgatg ctgatggccc aggaggccct ggcatctctg atggcccagg gggcaatgct 120
ggcgggccag gagaggcggg tgccacgggc gccagaggtc cccggggcgc aggggcagca 180
agggcctcgg gcccgagagg aggcgccccg cgggggtccgc atggcggtgc cgcttctgcg 240
caggatggaa ggtgcccctg cggggccagg aggcgggaca gccgcctgct tgagttgcac 300
atcacgatgc ctttctcgtc gcccatggaa gcggagctgg tccgcaggat cctgtcccgg 360
gatgccgcac cgctcccccg accaggggcg gttctgaagg acttcaccgt gtccggcaac 420
ctactgttta tgtcagttcg ggaccaggac agggaaggcg ctgggcggat gagggtggtg 480
ggttgggggc tgggatccgc ctccccggag gggcagaaag ctagagatct cagaacaccc 540
aaacacaagg tctcagaaca gagacctggt acaccaggcc cgccgccacc cgaggagacc 600
caggagatg ggtgcagagg tgtcgccctt aatgtgatgt tctctgcccc tcacatttag 660
ccgactgact gctgcagacc accgccaact gcagctctcc atcagctcct gtctccagca 720
gctttccctg ttgatgtgga tcacgcagtg ctttctgccc gtgttttttg ctcaggctcc 780
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aggaggacgg cttacatggt tgtttctgta gaaaataaag ctgagctacg aaaaaaaaaa 960
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 993

<210> 88
<211> 210
<212> PRT
<213> Homo sapiens

<400> 88

Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
1 5 10 15

Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
20 25 30

Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
35 40 45

Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro
50 55 60

His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala
65 70 75 80

Arg Arg Pro Asp Ser Arg Leu Leu Glu Leu His Ile Thr Met Pro Phe
85 90 95

Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp
100 105 110

Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val
115 120 125

Ser Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly
130 135 140

Ala Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser Pro
145 150 155 160

Glu Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser
165 170 175

Glu Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Pro Glu Gly Ala Gln
180 185 190

Gly Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala Pro
195 200 205

His Ile
210

<210> 89
<211> 236
<212> DNA
<213> Homo sapiens

<400> 89
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 cagagtctgg caccaacggg ctttgccaag tagctgctga gtgaatgggc acatgacgcc 120
 accctcagaa aggaaagcaa gatccggcgc accccctcag ggcgagcaaa accccatggg 180
 atccgcagag gaagcaggcc tagaatgcc cccaccacc cccagacaag cctgac 236

<210> 90
 <211> 47
 <212> PRT
 <213> Homo sapiens

<400> 90

Leu Leu Ser Glu Trp Ala His Asp Ala Thr Leu Arg Lys Glu Ser Lys
 1 5 10 15

Ile Arg Arg Thr Pro Ser Gly Arg Ala Lys Pro His Gly Ile Arg Arg
 20 25 30

Gly Ser Arg Pro Arg Met Pro Pro Thr His Pro Gln Thr Ser Leu
 35 40 45

<210> 91
 <211> 1584
 <212> DNA
 <213> Homo sapiens

<400> 91
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 ctgcccctgg cctgtcgcgc gcggctgctg ctgctgctgc tgtctctgct gccagtggcc 120
 agggcctcag aggctgagca ccgtctatct gagcggctgt ttgaagatta caatgagatc 180
 atccggcctg tagccaacgt gtctgaccca gtcacatcc atttcgaggt gtccatgtct 240
 cagctgggtga aggtggatga agtaaaccag atcatggaga ccaacctgtg gctcaagcaa 300
 atctggaatg actacaagct gaagtggaa cctctggct atggtggggc agagttcatg 360
 cgtgtccctg cacagaagat ctggaagcca gacattgtgc tgtataacaa tgctgttggg 420
 gatttccagg tgacgaccaa gaccaaagcc ttactcaagt aactgggga ggtgacttgg 480
 atacctccgg ccatctttaa gagtcctgt aaaatcgacg tgacctactt cccgtttgat 540
 taccaaaaact gtaccatgaa gttcggttcc tggctctacg ataaggcgaa aatcgatctg 600
 gtctgatcg gctcttccat gaacctcaag gactattggg agagcggcga gtgggccatc 660

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atcaaagccc caggctacaa acacgacatc aagtacaact gctgcgagga gatctacccc 720
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atccccctgcc tgctcatctc ctctctcaact gtgctcgtct tctacctgcc ctccgactgc 840
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atcactgaga ccatcccttc cacctcgtg gtcaccccc tgattggaga gtacctctg 960
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tatgttgcca tggtgattga tcgtatTTTT ctgtgggttt tcacctgggt gtgcattcta 1500
gggacagcag gattgtttct gcaacccctg atggccaggg aagatgcata agcactaagc 1560
tgtgtgcctg cctgggaaga cttc 1584

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<210> 92
<211> 502
<212> PRT
<213> Homo sapiens

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```

<400> 92

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```

Met Ala Leu Ala Val Ser Leu Pro Leu Ala Cys Arg Ala Arg Leu Leu
1           5           10           15

```

```

Leu Leu Leu Leu Ser Leu Leu Pro Val Ala Arg Ala Ser Glu Ala Glu
20           25           30

```

```

His Arg Leu Phe Glu Arg Leu Phe Glu Asp Tyr Asn Glu Ile Ile Arg
35           40           45

```

```

Pro Val Ala Asn Val Ser Asp Pro Val Ile Ile His Phe Glu Val Ser
50           55           60

```


Met Ser Gln Leu Val Lys Val Asp Glu Val Asn Gln Ile Met Glu Thr
65 70 75 80

Asn Leu Trp Leu Lys Gln Ile Trp Asn Asp Tyr Lys Leu Lys Trp Asn
85 90 95

Pro Ser Gly Tyr Gly Gly Ala Glu Phe Met Arg Val Pro Ala Gln Lys
100 105 110

Ile Trp Lys Pro Asp Ile Val Leu Tyr Asn Asn Ala Val Gly Asp Phe
115 120 125

Gln Val Thr Thr Lys Thr Lys Ala Leu Leu Lys Tyr Thr Gly Glu Val
130 135 140

Thr Trp Ile Pro Pro Ala Ile Phe Lys Ser Ser Cys Lys Ile Asp Val
145 150 155 160

Thr Tyr Phe Pro Phe Asp Tyr Gln Asn Cys Thr Met Lys Phe Gly Ser
165 170 175

Trp Ser Tyr Asp Lys Ala Lys Ile Asp Leu Val Leu Ile Gly Ser Ser
180 185 190

Met Asn Leu Lys Asp Tyr Trp Glu Ser Gly Glu Trp Ala Ile Ile Lys
195 200 205

Ala Pro Gly Tyr Lys His Asp Ile Lys Tyr Asn Cys Cys Glu Glu Ile
210 215 220

Tyr Pro Asp Ile Thr Tyr Ser Leu Tyr Ser Arg Arg Leu Pro Leu Phe
225 230 235 240

Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Phe Leu Thr
245 250 255

Val Leu Val Phe Tyr Leu Pro Ser Asp Cys Gly Glu Lys Val Thr Leu
260 265 270

Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Val Ile Thr
275 280 285

Glu Thr Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr
 290 295 300

Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Val Ile Thr Val
 305 310 315 320

Phe Val Leu Asn Val His Tyr Arg Thr Pro Thr Thr His Thr Met Pro
 325 330 335

Ser Trp Val Lys Thr Val Phe Leu Asn Leu Leu Pro Arg Val Met Phe
 340 345 350

Met Thr Arg Pro Thr Ser Asn Glu Gly Asn Ala Gln Lys Pro Arg Pro
 355 360 365

Leu Tyr Gly Ala Glu Leu Ser Asn Leu Asn Cys Phe Ser Arg Ala Glu
 370 375 380

Ser Lys Gly Cys Lys Glu Gly Tyr Pro Cys Gln Asp Gly Met Cys Gly
 385 390 395 400

Tyr Cys His His Arg Arg Ile Lys Ile Ser Asn Phe Ser Ala Asn Leu
 405 410 415

Thr Arg Ser Ser Ser Ser Glu Ser Val Asp Ala Val Val Ser Leu Ser
 420 425 430

Ala Leu Ser Pro Glu Ile Lys Glu Ala Ile Gln Ser Val Lys Tyr Ile
 435 440 445

Ala Glu Asn Met Lys Ala Gln Asn Glu Ala Lys Glu Ile Gln Asp Asp
 450 455 460

Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp Val Phe
 465 470 475 480

Thr Leu Val Cys Ile Leu Gly Thr Ala Gly Leu Phe Leu Gln Pro Leu
 485 490 495

Met Ala Arg Glu Asp Ala
 500

<210> 93
 <211> 515
 <212> DNA
 <213> Homo sapiens

<400> 93
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 ttttccctgg ggagagactt cactactatc tctgctgatg gactccatag ttctcatact 180
 ttacctgaaa gttcttcccta acatctgac tcaacctttc ttgccggggc attggcctgt 240
 tttcccagcc aagccttggt tttgtttttg aggaacgaac agcttttttg ggtacagacc 300
 aggagtccat gggctcttgag gacctctgtg tatttatcag ttttcttctc cacattcttt 360
 ttggcctgtc tccatagact tgtgagcccc atgccttggt taagggggaa aaatggcatt 420
 tccctacaaa ttaaatgtaa gaatccatag agaactggac cccattaaaa atatttggaa 480
 ttcacatggc cacttgatca tattccgctg gctca 515

<210> 94
 <211> 34
 <212> PRT
 <213> Homo sapiens

<400> 94

Met Ala Phe Pro Tyr Lys Leu Asn Val Arg Ile His Arg Glu Leu Asp
 1 5 10 15

Pro Ile Lys Asn Ile Trp Asn Ser His Gly His Leu Ile Ile Phe Arg
 20 25 30

Trp Leu

<210> 95
 <211> 490
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (439)..(439)
 <223> n = unknown

<400> 95

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caccagcct gtgctgtctt tattgaaaat agcaagcgat gattttccaa accagaaggc      180
caagcaggaa agcccagcgc gtcccttgcc ctcaaactca gctcttgggg aggtgtccag      240
tgacgtcctc tctgctgtac aggatgatcc caccctgatc gttaggaaga tgtgccccag      300
gaactcggga tttccttagt gtggtgatta ggggtgaaat ggatcctttg atagggagtt      360
tcttgatgga acgaagggcg agagtgtctc tgagaagtgc tgcagaccaa ggagggccag      420
cctgtcctgg agcacctgng gctgttcttg gagtaaggct gaagggccag aactgatgg      480
cttatggtgg                                     490

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<210> 96
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (94)..(94)
<223> X = unknown

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<400> 96

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```

Met Ile Phe Gln Thr Arg Arg Pro Ser Arg Lys Ala Gln Arg Val Pro
1           5           10           15

```

```

Cys Pro Gln Thr Gln Leu Leu Gly Arg Cys Pro Val Thr Ser Ser Leu
          20           25           30

```

```

Leu Tyr Arg Met Ile Pro Pro Arg Ser Leu Gly Arg Cys Ala Pro Gly
          35           40           45

```

```

Thr Arg Asp Phe Leu Ser Val Val Ile Arg Gly Glu Met Asp Pro Leu
50           55           60

```

```

Ile Gly Ser Phe Leu Met Glu Arg Arg Ala Arg Val Ser Leu Arg Ser
65           70           75           80

```

```

Ala Ala Asp Gln Gly Gly Pro Ala Cys Pro Gly Ala Pro Xaa Ala Val
          85           90           95

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Leu Gly Val Arg Leu Lys Gly Gln Thr Leu Met Ala Tyr Gly
 100 105 110

<210> 97
 <211> 3174
 <212> DNA
 <213> Homo sapiens

<400> 97
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<210> 98

<211> 700

<212> PRT

<213> Homo sapiens

<400> 98

Leu Thr Asp Asn Phe Ile Ala Ala Val Arg Arg Arg Asp Phe Ala Asn
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Met Thr Ser Leu Val His Leu Thr Leu Ser Arg Asn Thr Ile Gly Gln
20 25 30

Val Ala Ala Gly Ala Phe Ala Asp Leu Arg Ala Leu Arg Ala Leu His
35 40 45

Leu Asp Ser Asn Arg Leu Ala Glu Val Arg Gly Asp Gln Leu Arg Gly
50 55 60

Leu Gly Asn Leu Arg His Leu Ile Leu Gly Asn Asn Gln Ile Arg Arg
65 70 75 80

Val Glu Ser Ala Ala Phe Asp Ala Phe Leu Ser Thr Val Glu Asp Leu
85 90 95

Asp Leu Ser Tyr Asn Asn Leu Glu Ala Leu Pro Trp Glu Ala Val Gly
100 105 110

Gln Met Val Asn Leu Asn Thr Leu Thr Leu Asp His Asn Leu Ile Asp
115 120 125

His Ile Ala Glu Gly Thr Phe Val Gln Leu His Lys Leu Val Arg Leu
130 135 140

Asp Met Thr Ser Asn Arg Leu His Lys Leu Pro Pro Asp Gly Leu Phe
145 150 155 160

Leu Arg Ser Gln Gly Thr Gly Pro Lys Pro Pro Thr Pro Leu Thr Val
165 170 175

Ser Phe Gly Gly Asn Pro Leu His Cys Asn Cys Glu Leu Leu Trp Leu
 180 185 190

Arg Arg Leu Thr Arg Glu Asp Asp Leu Glu Thr Cys Ala Thr Pro Glu
 195 200 205

His Leu Thr Asp Arg Tyr Phe Trp Ser Ile Pro Glu Glu Glu Phe Leu
 210 215 220

Cys Glu Pro Pro Leu Ile Thr Arg Gln Ala Gly Gly Arg Ala Leu Val
 225 230 235 240

Val Glu Gly Gln Ala Val Ser Leu Arg Cys Arg Ala Val Gly Asp Pro
 245 250 255

Glu Pro Val Val His Trp Val Ala Pro Asp Gly Arg Leu Leu Gly Asn
 260 265 270

Ser Ser Arg Thr Arg Val Arg Gly Asp Gly Thr Leu Asp Val Thr Ile
 275 280 285

Thr Thr Leu Arg Asp Ser Gly Thr Phe Thr Cys Ile Ala Ser Asn Ala
 290 295 300

Ala Gly Glu Ala Thr Ala Pro Val Glu Val Cys Val Val Pro Leu Pro
 305 310 315 320

Leu Met Ala Pro Pro Pro Ala Ala Pro Pro Pro Leu Thr Glu Pro Gly
 325 330 335

Ser Ser Asp Ile Ala Thr Pro Gly Arg Pro Gly Ala Asn Asp Ser Ala
 340 345 350

Ala Glu Arg Arg Leu Val Ala Ala Glu Leu Thr Ser Asn Ser Val Leu
 355 360 365

Ile Arg Trp Pro Ala Gln Arg Pro Val Pro Gly Ile Arg Met Tyr Gln
 370 375 380

Val Gln Tyr Asn Ser Ser Val Asp Asp Ser Leu Val Tyr Arg Met Ile
 385 390 395 400

Pro Ser Thr Ser Gln Thr Phe Leu Val Asn Asp Leu Ala Ala Gly Arg
 405 410 415
 Ala Tyr Asp Leu Cys Val Leu Ala Val Tyr Asp Asp Gly Ala Thr Ala
 420 425 430
 Leu Pro Ala Thr Arg Val Val Gly Cys Val Gln Phe Thr Thr Ala Gly
 435 440 445
 Asp Pro Ala Pro Cys Arg Pro Leu Arg Ala His Phe Leu Gly Gly Thr
 450 455 460
 Met Ile Ile Ala Ile Gly Gly Val Ile Val Ala Ser Val Leu Val Phe
 465 470 475 480
 Ile Val Leu Leu Met Ile Arg Tyr Lys Val Tyr Gly Asp Gly Asp Ser
 485 490 495
 Arg Arg Val Lys Gly Ser Arg Ser Leu Pro Arg Val Ser His Val Cys
 500 505 510
 Ser Gln Thr Asn Gly Ala Gly Thr Gly Ala Ala Gln Ala Pro Ala Leu
 515 520 525
 Pro Ala Gln Asp His Tyr Glu Ala Leu Arg Glu Val Glu Ser Gln Ala
 530 535 540
 Ala Pro Ala Val Ala Val Glu Ala Lys Ala Met Glu Ala Glu Thr Ala
 545 550 555 560
 Ser Ala Glu Pro Glu Val Val Leu Gly Arg Ser Leu Gly Gly Ser Ala
 565 570 575
 Thr Ser Leu Cys Leu Leu Pro Ser Glu Glu Thr Ser Gly Glu Glu Ser
 580 585 590
 Arg Ala Ala Val Gly Pro Arg Arg Ser Arg Ser Gly Ala Leu Glu Pro
 595 600 605
 Pro Thr Ser Ala Pro Pro Thr Leu Ala Leu Val Pro Gly Gly Ala Ala
 610 615 620

Ala Arg Pro Arg Pro Gln Gln Arg Tyr Ser Phe Asp Gly Asp Tyr Gly
625 630 635 640

Ala Leu Phe Gln Ser His Ser Tyr Pro Arg Arg Ala Arg Arg Thr Lys
645 650 655

Arg His Arg Ser Thr Pro His Leu Asp Gly Ala Gly Gly Gly Ala Ala
660 665 670

Gly Glu Asp Gly Asp Leu Gly Leu Gly Ser Ala Arg Ala Cys Leu Ala
675 680 685

Phe Thr Ser Thr Glu Trp Met Leu Glu Ser Thr Val
690 695 700

<210> 99
<211> 697
<212> DNA
<213> Homo sapiens

<400> 99
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ctggaggcct ggcaggacga catgcagggtg gtgatcgggc agcagctgcy ctcacagcgc 180
cagaaggagc tgagcgcctc cgcgtcgtcg tcgaccccgcc gccgtgccgc gccccgcttc 240
tcgccgcgcc tgggccccgg gcccgccggt ggcttttctca gtaacctctt ccgaaggacc 300
tgacggctgg gccagaggg ctgcccttgc ccacttaggg gctcactttc ctcttcaggc 360
caatggagcg acagggccca gattgtcttc caaaagaagc tgatgccctc cccgccccag 420
gatgctgggc aagggtcat cgggagcagg ggctcatccg gagcaggggc cagctttgtg 480
gggcaggagc tccaggtggg tggcaggggc aggtgaacag agctattttc cgaattaata 540
taggtctatc ttttctaggg cagggatggg gctgggtatt tatgtatcaa gatcggacag 600
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<210> 100
<211> 100
<212> PRT
<213> Homo sapiens

<400> 100

Glu Ala Val Asn Lys Ala Leu Glu Leu Ser Leu Gln Leu Asn Arg Val
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Ser Leu Glu Arg Asp Ser Leu Ser Arg Glu Leu Leu Arg Ala Ile Arg
 20 25 30

Gln Lys Val Ala Leu Thr Gln Glu Leu Glu Ala Trp Gln Asp Asp Met
 35 40 45

Gln Val Val Ile Gly Gln Gln Leu Arg Ser Gln Arg Gln Lys Glu Leu
 50 55 60

Ser Ala Ser Ala Ser Ser Ser Thr Pro Arg Arg Ala Ala Pro Arg Phe
 65 70 75 80

Ser Pro Arg Leu Gly Pro Gly Pro Ala Gly Gly Phe Leu Ser Asn Leu
 85 90 95

Phe Arg Arg Thr
 100

<210> 101

<211> 302

<212> DNA

<213> Homo sapiens

<400> 101

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 aaaccttttg cctctagaag atatatcaat taacacacaa tattcaagga aatcagtgct 240
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<210> 102

<211> 38

<212> PRT

<213> Homo sapiens

<400> 102

Leu Pro Leu Glu Asp Ile Ser Ile Asn Thr Gln Tyr Ser Arg Lys Ser
 1 5 10 15

Val Leu Tyr Arg Tyr Phe Trp Ser Ile Lys Val Gln Phe Ile Ile Gln
 20 25 30

Asn Gln His Asn Thr Glu
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<210> 103

<211> 1628

<212> DNA

<213> Homo sapiens

<400> 103

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ccatggtacc ccaggcagtg aggcgggacc agaagagctg aatacttctg tctaccagcc      180
catagatgga tcaccagatt atcagaaagc aaaattacaa gttcttgggg ccatccagat      240
cctgaatgca gcaatgattc tggctttggg tgtctttctg ggttccttgc aatacccata      300
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aaaaaaaaa 1628

```

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<210> 104
<211> 214
<212> PRT
<213> Homo sapiens
<400> 104

```

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Met Ala Ser His Glu Val Asp Asn Ala Glu Leu Gly Ser Ala Ser Ala
1          5          10          15

```

```

His Gly Thr Pro Gly Ser Glu Ala Gly Pro Glu Glu Leu Asn Thr Ser
          20          25          30

```

```

Val Tyr Gln Pro Ile Asp Gly Ser Pro Asp Tyr Gln Lys Ala Lys Leu
          35          40          45

```

```

Gln Val Leu Gly Ala Ile Gln Ile Leu Asn Ala Ala Met Ile Leu Ala
50          55          60

```

```

Leu Gly Val Phe Leu Gly Ser Leu Gln Tyr Pro Tyr His Phe Gln Lys
65          70          75          80

```

```

His Phe Phe Phe Phe Thr Phe Tyr Thr Gly Tyr Pro Ile Trp Gly Ala
          85          90          95

```

```

Val Phe Phe Cys Ser Ser Gly Thr Leu Ser Val Val Ala Gly Ile Lys
100          105          110

```

```

Pro Thr Arg Thr Trp Ile Gln Asn Ser Phe Gly Met Asn Ile Ala Ser
115          120          125

```

Ala Thr Ile Ala Leu Val Gly Thr Ala Phe Leu Ser Leu Asn Ile Ala
130 135 140

Val Asn Ile Gln Ser Leu Arg Ser Cys His Ser Ser Ser Glu Ser Pro
145 150 155 160

Asp Leu Cys Asn Tyr Met Gly Ser Ile Ser Asn Gly Met Val Ser Leu
165 170 175

Leu Leu Ile Leu Thr Leu Leu Glu Leu Cys Val Thr Ile Ser Thr Ile
180 185 190

Ala Met Trp Cys Asn Ala Asn Cys Cys Asn Ser Arg Glu Glu Ile Ser
195 200 205

Ser Pro Pro Asn Ser Val
210

<210> 105

<211> 2011

<212> DNA

<213> Homo sapiens

<400> 105

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<210> 106

<211> 530

<212> PRT

<213> Homo sapiens

<400> 106

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Met Asp Ile Lys Asn Ser Pro Ser Ser Leu Asn Ser Pro Ser Ser Tyr
1           5           10           15

```

```

Asn Cys Ser Gln Ser Ile Leu Pro Leu Glu His Gly Ser Ile Tyr Ile
20           25           30

```

Pro Ser Ser Tyr Val Asp Ser His His Glu Tyr Pro Ala Met Thr Phe
 35 40 45
 Tyr Ser Pro Ala Val Met Asn Tyr Ser Ile Pro Ser Asn Val Thr Asn
 50 55 60
 Leu Glu Gly Gly Pro Gly Arg Gln Thr Thr Ser Pro Asn Val Leu Trp
 65 70 75 80
 Pro Thr Pro Gly His Leu Ser Pro Leu Val Val His Arg Gln Leu Ser
 85 90 95
 His Leu Tyr Ala Glu Pro Gln Lys Ser Pro Trp Cys Glu Ala Arg Ser
 100 105 110
 Leu Glu His Thr Leu Pro Val Asn Arg Glu Thr Leu Lys Arg Lys Val
 115 120 125
 Ser Gly Asn Arg Cys Ala Ser Pro Val Thr Gly Pro Gly Ser Lys Arg
 130 135 140
 Asp Ala His Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His
 145 150 155 160
 Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser
 165 170 175
 Ile Gln Gly His Asn Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr
 180 185 190
 Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys
 195 200 205
 Cys Tyr Glu Val Gly Met Val Lys Cys Gly Ser Arg Arg Glu Arg Cys
 210 215 220
 Gly Tyr Arg Leu Val Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His
 225 230 235 240
 Cys Ala Gly Lys Ala Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg
 245 250 255

Glu Leu Leu Leu Asp Ala Leu Ser Pro Glu Gln Leu Val Leu Thr Leu
 260 265 270

Leu Glu Ala Glu Pro Pro His Val Leu Ile Ser Arg Pro Ser Ala Pro
 275 280 285

Phe Thr Glu Ala Ser Met Met Met Ser Leu Thr Lys Leu Ala Asp Lys
 290 295 300

Glu Leu Val His Met Ile Ser Trp Ala Lys Lys Ile Pro Gly Phe Val
 305 310 315 320

Glu Leu Ser Leu Phe Asp Gln Val Arg Leu Leu Glu Ser Cys Trp Met
 325 330 335

Glu Val Leu Met Met Gly Leu Met Trp Arg Ser Ile Asp His Pro Gly
 340 345 350

Lys Leu Ile Phe Ala Pro Asp Leu Val Leu Asp Arg Asp Glu Gly Lys
 355 360 365

Cys Val Glu Gly Ile Leu Glu Ile Phe Asp Met Leu Leu Ala Thr Thr
 370 375 380

Ser Arg Phe Arg Glu Leu Lys Leu Gln His Lys Glu Tyr Leu Cys Val
 385 390 395 400

Lys Ala Met Ile Leu Leu Asn Ser Ser Met Tyr Pro Leu Val Thr Ala
 405 410 415

Thr Gln Asp Ala Asp Ser Ser Arg Lys Leu Ala His Leu Leu Asn Ala
 420 425 430

Val Thr Asp Ala Leu Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser
 435 440 445

Gln Gln Gln Ser Met Arg Leu Ala Asn Leu Leu Met Leu Leu Ser His
 450 455 460

Val Arg His Ala Ser Asn Lys Gly Met Glu His Leu Leu Asn Met Lys
 465 470 475 480

Cys Lys Asn Val Val Pro Val Tyr Asp Leu Leu Leu Glu Met Leu Asn
 485 490 495

Ala His Val Leu Arg Gly Cys Lys Ser Ser Ile Thr Gly Ser Glu Cys
 500 505 510

Ser Pro Ala Glu Asp Ser Lys Ser Lys Glu Gly Ser Gln Asn Pro Gln
 515 520 525

Ser Gln
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 <213> Homo sapiens

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<210> 108
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<212> PRT
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<400> 108

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Arg Val Leu Cys Cys Glu Thr Pro Arg Gly Cys Pro Val Thr Ser Val
20           25           30

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Thr Pro Tyr Gly Thr Ser Pro Thr Asn Ala Leu Tyr Pro Ser Leu Ser
35           40           45

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Thr Ser Met Val Ser Ala Ser Val Ala Ser Thr Ser Val Ala Ser Ser
50           55           60

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Ser Val Ala Ser Ser Ser Val Ala Tyr Ser Thr Gln Thr Cys Phe Cys
65           70           75           80

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Asn Val Ala Asp Arg Leu Tyr Pro Ala Gly Ser Thr Ile Tyr Arg His
85           90           95

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Arg Asp Leu Ala Gly His Cys Tyr Tyr Ala Leu Cys Ser Gln Asp Cys
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Gln Val Val Arg Gly Val Asp Ser Asp Cys Arg Ser Thr Thr Leu Pro
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 Glu Leu Gly Cys Pro Asn Ala Val Pro Pro Arg Lys Lys Gly Glu Thr
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 Trp Ala Thr Pro Asn Cys Ser Glu Ala Thr Cys Glu Gly Asn Asn Val
 165 170 175
 Ile Ser Leu Ser Pro Arg Thr Cys Pro Arg Val Glu Lys Pro Thr Cys
 180 185 190
 Ala Asn Gly Tyr Pro Ala Val Lys Val Ala Asp Gln Asp Gly Cys Cys
 195 200 205
 His His Tyr Gln Cys Gln Cys Val Cys Ser Gly Trp Gly Asp Pro His
 210 215 220
 Tyr Ile Thr Phe Asp Gly Thr Tyr Tyr Thr Phe Leu Asp Asn Cys Thr
 225 230 235 240
 Tyr Val Leu Val Gln Gln Ile Val Pro Val Tyr Gly His Phe Arg Val
 245 250 255
 Leu Val Asp Asn Tyr Phe Cys Gly Ala Glu Asp Gly Leu Ser Cys Pro
 260 265 270
 Arg Ser Ile Ile Leu Glu Tyr His Gln Asp Arg Val Val Leu Thr Arg
 275 280 285
 Lys Pro Val His Gly Val Met Thr Asn Glu Ile Ile Phe Asn Asn Lys
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 Val Val Ser Pro Ala Phe Arg Lys Asn Gly Ile Val Val Ser Arg Ile
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 Gly Val Lys Met Tyr Ala Thr Ile Pro Glu Leu Gly Val Gln Val Met
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Phe Ser Gly Leu Ile Phe Ser Val Glu Val Pro Phe Ser Lys Phe Ala
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 Asn Asn Thr Glu Gly Gln Cys Gly Thr Cys Thr Asn Asp Arg Lys Asp
 355 360 365
 Glu Cys Arg Thr Pro Arg Gly Thr Val Val Ala Ser Cys Ser Glu Met
 370 375 380
 Ser Gly Leu Trp Asn Val Ser Ile Pro Asp Gln Pro Ala Cys His Arg
 385 390 395 400
 Pro His Pro Thr Pro Thr Thr Val Gly Pro Thr Thr Val Gly Ser Thr
 405 410 415
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 Pro Pro Ala Pro Cys Leu Pro Ser Pro Ile Cys His Leu Ile Leu Ser
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 Lys Val Phe Glu Pro Cys His Thr Val Ile Pro Pro Leu Leu Phe Tyr
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 Glu Gly Cys Val Phe Asp Arg Cys His Met Thr Asp Leu Asp Val Val
 465 470 475 480
 Cys Ser Ser Leu Glu Leu Tyr Ala Ala Leu Cys Ala Ser His Asp Ile
 485 490 495
 Cys Ile Asp Trp Arg Gly Arg Thr Gly His Met Cys Pro Phe Thr Cys
 500 505 510
 Pro Ala Asp Lys Val Tyr Gln Pro Cys Gly Pro Ser Asn Pro Ser Tyr
 515 520 525
 Cys Tyr Gly Asn Asp Ser Ala Ser Leu Gly Ala Leu Pro Glu Ala Gly
 530 535 540
 Pro Ile Thr Glu Gly Cys Phe Cys Pro Glu Gly Met Thr Leu Phe Ser
 545 550 555 560

Thr Ser Ala Gln Val Cys Val Pro Thr Gly Cys Pro Arg Cys Leu Gly
 565 570 575

Pro His Gly Glu Pro Val Lys Val Gly His Thr Val Gly Met Asp Cys
 580 585 590

Gln Glu Cys Thr Cys Glu Ala Ala Thr Trp Thr Leu Thr Cys Arg Pro
 595 600 605

Lys Leu Cys Pro Leu Pro Pro Ala Cys Pro Leu Pro Gly Phe Val Pro
 610 615 620

Val Pro Ala Ala Pro Gln Ala Gly Gln Cys Cys Pro Gln Tyr Ser Cys
 625 630 635 640

Ala Cys Asn Thr Ser Arg Cys Pro Ala Pro Val Gly Cys Pro Glu Gly
 645 650 655

Ala Arg Ala Ile Pro Thr Tyr Gln Glu Gly Ala Cys Cys Pro Val Gln
 660 665 670

Asn Cys Ser Trp Thr Val Cys Ser Ile Asn Gly Thr Leu Tyr Gln Pro
 675 680 685

Gly Ala Val Val Ser Ser Ser Leu Cys Glu Thr Cys Arg Cys Glu Leu
 690 695 700

Pro Gly Gly Pro Pro Ser Asp Ala Phe Val Val Ser Cys Glu Thr Gln
 705 710 715 720

Ile Cys Asn Thr His Cys Pro Val Gly Phe Glu Tyr Gln Glu Gln Ser
 725 730 735

Gly Gln Cys Cys Gly Thr Cys Val Gln Val Ala Cys Val Thr Asn Thr
 740 745 750

Ser Lys Ser Pro Ala His Leu Phe Tyr Pro Gly Glu Thr Trp Ser Asp
 755 760 765

Ala Gly Asn His Cys Val Thr His Gln Cys Glu Lys His Gln Asp Gly
 770 775 780

Leu Val Val Val Thr Thr Lys Lys Ala Cys Pro Pro Leu Ser Cys Ser
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 Leu Asp Glu Ala Arg Met Ser Lys Asp Gly Cys Cys Arg Phe Cys Pro
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 Leu Pro Pro Pro Pro Tyr Gln Asn Gln Ser Thr Cys Ala Val Tyr His
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 Arg Ser Leu Ile Ile Gln Gln Gln Gly Cys Ser Ser Ser Glu Pro Val
 835 840 845
 Arg Leu Ala Tyr Cys Arg Gly Asn Cys Gly Asp Ser Ser Ser Met Tyr
 850 855 860
 Ser Leu Glu Gly Asn Thr Val Glu His Arg Cys Gln Cys Cys Gln Glu
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 885 890 895
 Ser Arg Ala Phe Ser Tyr Thr Glu Val Glu Glu Cys Gly Cys Met Gly
 900 905 910
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 915 920 925
 Pro Glu Pro Ser Gln Glu Ala Glu Ser Gly Ser Trp Glu Arg Gly Val
 930 935 940
 Gln Cys Pro Pro Cys Thr Asp Gln His Cys Arg Pro Pro Asp Leu Gln
 945 950 955 960
 Gly Glu Pro Pro Ile Cys Pro Leu Ser Ser Ala Ser Lys Ala Ser Gly
 965 970 975
 Thr Cys Ala Pro Val Gln Ala Ala Ala Ala Leu Asn Thr Leu Ser Thr
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 Pro Ala Phe Leu Trp Arg Val Trp Ala Met Gly His Leu Leu Pro Gly
 995 1000 1005

Gly Gly Ala Leu Thr His Pro Ala Cys Ser His Leu Ser Gly Pro
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Ala Pro Gly Leu Ala Glu Leu Leu Trp Pro Cys Ile Gln Pro Ala
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Val Leu Gly Thr
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Trp Pro Glu Ser Val Gln Ser Trp Leu Leu Gly Thr Ala Pro Ala Leu
35 40 45

Gly Cys His Ser Ser Asp Gln Asp Thr Gln Leu Leu Leu Leu Gln Trp
50 55 60

Gln Glu Glu Leu Gln His Glu Leu Lys Val Asn Asn Gln Ala Glu His
65 70 75 80

Gln Gly Glu Arg Arg Ala Arg Ile Leu Arg Val Asn Ser Gly Cys Arg
85 90 95

Ala Gly Arg Ala Leu Gly Ala Thr Leu Leu Arg Leu Gly Val Asn Asp
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Gln Glu Gly Gly Met His Xaa Xaa Thr Gly Ser Glu Lys Glu Arg
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<212> DNA
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<210> 112
<211> 573
<212> PRT
<213> Homo sapiens

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<400> 112

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Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys Leu Leu Asp
          20          25          30

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Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu Asn Tyr Lys
          35          40          45

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Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp Val Ile Leu
          50          55          60

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Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg Glu Ile His
          65          70          75          80

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Gln Glu Thr His Pro Asp Ser Glu Thr Ala Phe Glu Ile Lys Ser Ser
          85          90          95

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Val Ser Ser Arg Ser Ile Phe Lys Asp Lys Gln Ser Cys Asp Ile Lys
          100          105          110

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Met Glu Gly Met Ala Arg Asn Asp Leu Trp Tyr Leu Ser Leu Glu Glu
          115          120          125

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Val Trp Lys Cys Arg Asp Gln Leu Asp Lys Tyr Gln Glu Asn Pro Glu
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 Arg His Leu Arg Gln Val Ala Phe Thr Gln Lys Lys Val Leu Thr Gln
 145 150 155 160
 Glu Arg Val Ser Glu Ser Gly Lys Tyr Gly Gly Asn Cys Leu Leu Pro
 165 170 175
 Ala Gln Leu Val Leu Arg Glu Tyr Phe His Lys Arg Asp Ser His Thr
 180 185 190
 Lys Ser Leu Lys His Asp Leu Val Leu Asn Gly His Gln Asp Ser Cys
 195 200 205
 Ala Ser Asn Ser Asn Glu Cys Gly Gln Thr Phe Cys Gln Asn Ile His
 210 215 220
 Leu Ile Gln Phe Ala Arg Thr His Thr Gly Asp Lys Ser Tyr Lys Cys
 225 230 235 240
 Pro Asp Asn Asp Asn Ser Leu Thr His Gly Ser Ser Leu Gly Ile Ser
 245 250 255
 Lys Gly Ile His Arg Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys
 260 265 270
 Phe Phe Ser Trp Arg Ser Asn Leu Thr Arg His Gln Leu Ile His Thr
 275 280 285
 Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ser Phe Ser Arg
 290 295 300
 Ser Ser His Leu Ile Gly His Gln Lys Thr His Thr Gly Glu Glu Pro
 305 310 315 320
 Tyr Glu Cys Lys Glu Cys Gly Lys Ser Phe Ser Trp Phe Ser His Leu
 325 330 335
 Val Thr His Gln Arg Thr His Thr Gly Asp Lys Leu Tyr Thr Cys Asn
 340 345 350

Gln Cys Gly Lys Ser Phe Val His Ser Ser Arg Leu Ile Arg His Gln
 355 360 365

Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Pro Glu Cys Gly Lys
 370 375 380

Ser Phe Arg Gln Ser Thr His Leu Ile Leu His Gln Arg Thr His Val
 385 390 395 400

Arg Val Arg Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ser Tyr Ser Gln
 405 410 415

Arg Ser His Leu Val Val His His Arg Ile His Thr Gly Leu Lys Pro
 420 425 430

Phe Glu Cys Lys Asp Cys Gly Lys Cys Phe Ser Arg Ser Ser His Leu
 435 440 445

Tyr Ser His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys His
 450 455 460

Asp Cys Gly Lys Ser Phe Ser Gln Ser Ser Ala Leu Ile Val His Gln
 465 470 475 480

Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Cys Gln Cys Gly Lys
 485 490 495

Ala Phe Ile Arg Lys Asn Asp Leu Ile Lys His Gln Arg Ile His Val
 500 505 510

Gly Glu Glu Thr Tyr Lys Cys Asn Gln Cys Gly Ile Ile Phe Ser Gln
 515 520 525

Asn Ser Pro Phe Ile Val His Gln Ile Ala His Thr Gly Glu Gln Phe
 530 535 540

Leu Thr Cys Asn Gln Cys Gly Thr Ala Leu Val Asn Thr Ser Asn Leu
 545 550 555 560

Ile Gly Tyr Gln Thr Asn His Ile Arg Glu Asn Ala Tyr
 565 570

<210> 113
 <211> 1130
 <212> DNA
 <213> Homo sapiens

<400> 113
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 aagaagcgct agtaaggtct ctgagatcct tgcactagct acatcctcag ggtaggagga 120
 agatggcttc cagaagcatg cggctgctcc tattgctgag ctgcctggcc aaaacaggag 180
 tcctgggtga tatcatcatg agaccagct gtgctcctgg atggttttac cacaagtcca 240
 attgctatgg ttacttcagg aagctgagga actggtctga tgccgagctc gagtgtcagt 300
 cttacggaaa cggagccac ctggcatcta tcctgagttt aaaggaagcc agcaccatag 360
 cagagtacat aagtggctat cagagaagcc agccgatatg gattggcctg cacgaccac 420
 agaagaggca gcagtggcag tggattgatg gggccatgta tctgtacaga tcctgggtctg 480
 gcaagtccat gggtggaac aagcactgtg ctgagatgag ctccaataac aacttttta 540
 cttggagcag caacgaatgc aacaagcgcc aacacttcct gtgcaagtac cgaccataga 600
 gcaagaatca agattctgct aactcctgca cagccccgtc ctcttccttt ctgctagcct 660
 ggctaaatct gctcattatt tcagagggga aacctagcaa actaagagtg ataagggccc 720
 tactacactg gcttttttag gcttagagac agaaacttta gcattggccc agtagtggct 780
 tctagctcta aatgtttgcc cgcctatccc ttccacagt atccttcttc cctcctcccc 840
 tgtctctggc tgtctcgagc agtctagaag agtgcattc cagcctatga aacagctggg 900
 tctttggcca taagaagtaa agatttgaag acagaaggaa gaaactcagg agtaagcttc 960
 tagaccctt cagcttctac acccttctgc cctctctcca ttgcctgcac cccacccag 1020
 ccactcaact cctgcttgtt tttcctttgg ccataggaag gtttaccagt agaatccttg 1080
 ctaggttgat gtgggccata cattccttta ataaaccatt gtgtacataa 1130

<210> 114
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 114

Met Ala Ser Arg Ser Met Arg Leu Leu Leu Leu Leu Ser Cys Leu Ala
 1 5 10 15

Lys Thr Gly Val Leu Gly Asp Ile Ile Met Arg Pro Ser Cys Ala Pro
20 25 30

Gly Trp Phe Tyr His Lys Ser Asn Cys Tyr Gly Tyr Phe Arg Lys Leu
35 40 45

Arg Asn Trp Ser Asp Ala Glu Leu Glu Cys Gln Ser Tyr Gly Asn Gly
50 55 60

Ala His Leu Ala Ser Ile Leu Ser Leu Lys Glu Ala Ser Thr Ile Ala
65 70 75 80

Glu Tyr Ile Ser Gly Tyr Gln Arg Ser Gln Pro Ile Trp Ile Gly Leu
85 90 95

His Asp Pro Gln Lys Arg Gln Gln Trp Gln Trp Ile Asp Gly Ala Met
100 105 110

Tyr Leu Tyr Arg Ser Trp Ser Gly Lys Ser Met Gly Gly Asn Lys His
115 120 125

Cys Ala Glu Met Ser Ser Asn Asn Asn Phe Leu Thr Trp Ser Ser Asn
130 135 140

Glu Cys Asn Lys Arg Gln His Phe Leu Cys Lys Tyr Arg Pro
145 150 155

<210> 115
<211> 447
<212> DNA
<213> Homo sapiens

<400> 115
cccgtcttga cacaccgcag ctgacaagga gaagtaaaat agggcaccca aactactctg 60
cgctttaccc tctcaaacac ttgtttttaa atcctttgca tctagtcagt cattcaacat 120
gtatcaagca ccagcagcta ttcgtagcac agctgttaag acctggaata ataaaacctt 180
aagactatatt ggcaacttac tcctgaaagg taatatacgg ataatttcac ctgtaacacg 240
cagatgagga aattgacctc acagatttaa tgtaaattca gagtttacac caatttaacc 300
gcaacaaata aggagctgtc aatatatatt taataaggaa cacacaaaaa aaaagctgaa 360
taaataccact tcttaccttc tgctccagtt gcctctgccca gctggtgaaa gcttaaggag 420

ctgagccctc ttagcctcga ggatgag

447

<210> 116
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 116

Arg Leu Asp Thr Pro Gln Leu Thr Arg Arg Ser Lys Ile Gly His Pro
 1 5 10 15

Asn Tyr Ser Ala Leu Tyr Pro Leu Lys His Leu Phe Leu Asn Pro Leu
 20 25 30

His Leu Val Ser His Ser Thr Cys Ile Lys His Gln Gln Leu Phe Val
 35 40 45

Ala Gln Leu Leu Arg Pro Gly Ile Ile Lys Pro
 50 55

<210> 117
 <211> 319
 <212> DNA
 <213> Homo sapiens

<400> 117

ggtgaagctc ccagccatca gccatgaggg tcttgatatct cctcttctcg ttcctcttca 60
 tattcctgat gcctcttcca ggtgtttttg gtggtatagg cgatcctgtt acctgcctta 120
 agagtggagc catatgtcat ccagtctttt gccctagaag gtataaacia attggcacct 180
 gtggtctccc tggaacaaaa tgctgcaaaa agccatgagg aggccaagaa gctgctgtgg 240
 ctgatgcgga ttcagaaagg gctccctcat cagagacgtg cgacatgtaa accaaattaa 300
 actatgggtgt ccaaagata 319

<210> 118
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 118

Met Arg Val Leu Tyr Leu Leu Phe Ser Phe Leu Phe Ile Phe Leu Met
 1 5 10 15

Pro Leu Pro Gly Val Phe Gly Gly Ile Gly Asp Pro Val Thr Cys Leu
20 25 30

Lys Ser Gly Ala Ile Cys His Pro Val Phe Cys Pro Arg Arg Tyr Lys
35 40 45

Gln Ile Gly Thr Cys Gly Leu Pro Gly Thr Lys Cys Cys Lys Lys Pro
50 55 60

<210> 119
<211> 582
<212> DNA
<213> Homo sapiens

<400> 119
ggggggccaaa caccttcctg acaccatgag ggccagcagc ttcttgatcg tgggtggtgtt 60
cctcatcgct gggacgctgg ttctagaggc agctgtcacg ggagttcctg ttaaagggtca 120
agacactgtc aaaggccgtg ttccattcaa tggacaagat cccgttaaag gacaagtttc 180
agttaaagggt caagataaag tcaaagcgca agagccagtc aaagggtccag tctccactaa 240
gcctggctcc tgccccatta tcttgatccg gtgcgccatg ttgaatcccc ctaaccgctg 300
cttgaaagat actgactgcc caggaatcaa gaagtgtgt gaaggctctt gcgggatggc 360
ctgtttcgtt cccagtgag agggagccgg tccttgctgc acctgtgccg tccccagagc 420
tacaggctcc atctggctct aagtcctgc tgcccttccc ctccacac tgtccattct 480
tcctccatt caggatgccc acggctggag ctgcctctct catccacttt ccaataaaga 540
gttccttctg caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 582

<210> 120
<211> 117
<212> PRT
<213> Homo sapiens

<400> 120

Met Arg Ala Ser Ser Phe Leu Ile Val Val Val Phe Leu Ile Ala Gly
1 5 10 15

Thr Leu Val Leu Glu Ala Ala Val Thr Gly Val Pro Val Lys Gly Gln
20 25 30

Asp Thr Val Lys Gly Arg Val Pro Phe Asn Gly Gln Asp Pro Val Lys
35 40 45

Gly Gln Val Ser Val Lys Gly Gln Asp Lys Val Lys Ala Gln Glu Pro
50 55 60

Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys Pro Ile Ile Leu
65 70 75 80

Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys Leu Lys Asp Thr
85 90 95

Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser Cys Gly Met Ala
100 105 110

Cys Phe Val Pro Gln
115

<210> 121

<211> 3005

<212> DNA

<213> Homo sapiens

<400> 121

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cagggcacct cgctccctcg cctctggcag cgggaccctg tgggcattga aatccaactc	120
actcatgctt atttcctgta atggacaaac ttgatgctaa tgtgagttct gaggagggtt	180
tggggtcagt ggagaagggtg gtgctgctca cgtttctctc gacggttatc ctgatggcca	240
tcttggggaa cctgctggtg atggtggctg tgtgctggga caggcagctc agggaaataa	300
aaacaaatta tticattgta tctcttgctt ttgcggatct gctggtttctg gtgctggtga	360
tgcccttttg tgccattgag ctgggttcaag acatctggat ttatggggag gtgttttctc	420
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cccctctgcg catcgcatca atgctgggag gctgctgggt catccccacg tttatttctt	600
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agttcaacca gaactctaac tctacgtact gtgtcttcat ggtcaacaag ccctacgcca	720
tcacctgctc tgtggtggcc ttctacatcc catttctcct catggtgctg gcctattacc	780
gcatctatgt cacagctaag gagcatgccc atcagatcca gatgttataa cgggcaggag	840
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agaccaaagc agccaagacc ctgtgcatca tcatggggtg cttctgcctc tgctgggcac	960
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cgccagcaac ttctcctttg gtggctgctc agcccagtga cacttaggcc cctgggacaa	1320
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cactcacgtt ctaagcacga tagcttgctg cgtcctatct cggtcactga tgtctccaaa	1680
tacgccttct ttgctgtgtg ggcttccaga tatcaacaaa atactccctc tctgttccctg	1740
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gtccacttgc tcttccttat gtccaatgtc tgtcctctc ttcaggacat gctccattta	1980
ttttccatgg aagacacagg gtcagagatc tgtcagagga aaatggtctc cacagcaact	2040
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cacactgggg aaactcattt tcccctgcag ctcccccaag gtgcaggagg gcaggatcca	2340
gcagcactgg ggatgccgag gcaatgctgt acttgaagcc agaggaccca aattgccgcc	2400
ctggctgtgc tgcaaacaag ctgtgagatc ttgaatagt ttctttcatc tctggacccc	2460
actttccaca tctgtgcact caagcttggga ctagaggacc tttaagtttt ctttctgttt	2520
ctaagacaac agtatgctgc tatagccgtc tgctacctcg agaagccatg gcctgcctgc	2580

cttttggcctt	tgtttcaaag	gaacgaccct	cctcatttgg	gcctttttaga	cccctgacct	2640
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cttgcaatg	ccccatagca	gaagtcccgg	gaaggtaa	gccaaacca	gagccatgtg	2760
agattctgac	tttgatcttg	gctgtggtt	aatagcatct	caggattatt	tatcatattc	2820
tctttttt	ttattgctta	taagggtgtca	gttattgtt	ccattgttgt	ttactttagt	2880
tctggaactg	aaaccgacag	gaagaaactt	tggaataagg	aagagaagat	tgaccaaacc	2940
atccaaatgc	caaaaagraa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaagcggc	3000
cgctg						3005

<210> 122
 <211> 1328
 <212> DNA
 <213> Homo sapiens

<400> 122	
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ggacaaactt	gatgctaattg
tgagttctga	ggaggggtttc
60	
gggtcagtgg	agaagggtgg
gctgctcacg	tttctctcga
cggttatcct	gatggccatc
120	
ttggggaacc	tgctgggtgat
ggtggctgtg	tgctgggaca
ggcagctcag	gaaaataaaa
180	
acaaattatt	tcattgtatc
tcttgctttt	gcggatctgc
tggtttcggt	gctgggtgatg
240	
ccctttgggtg	ccattgagct
ggttcaagac	atctggattt
atggggaggt	gttttgtctt
300	
gttcggacat	ctctggacgt
cctgctcaca	acggcatcga
tttttcacct	gtgctgcatt
360	
tctctggata	ggtattacgc
catctgctgc	cagcctttgg
tctataggaa	caagatgacc
420	
cctctgogca	tcgcattaat
gctggggaggc	tgctgggtca
tccccacgtt	tatttctttt
480	
ctccctataa	tgcaaggctg
gaataacatt	ggcataattg
atctgataga	aaagaggaag
540	
ttcaaccaga	actctaactc
tacgtactgt	gtcttcatgg
tcaacaagcc	ctacgccatc
600	
acctgctctg	tggtggcctt
ctacatccca	tttctcctca
tggtgctggc	ctattaccgc
660	
atctatgtca	cagctaagga
gcatgcccat	cagatccaga
tggttacaacg	ggcaggagcc
720	
tctctcgaga	gcaggcctca
gtcggcagac	cagcatagca
ctcatcgcat	gaggacagag
780	
accaaagcag	ccaagaccct
gtgcatcatc	atgggttgct
tctgcctctg	ctgggcacca
840	
ttctttgtca	ccaatattgt
ggatcctttc	atagactaca
ctgtccctgg	gcagggtgtg
900	
actgctttcc	tctggctcgg
ctatatcaat	tccgggttga
acccttttct	ctacgccttc
960	
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tgcttctctc	atcatcctct
gctgtgatga	tgagcgctac
1020	

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 acacatgtac taagggatgc agtggagtgt ggtggccagt gggagagtca gtgtcaccgc 1140
 ccagcaactt ctcctttggg ggctgctcag ccagtgaca cttaggcccc tgggacaatg 1200
 acccagaaga cagccatgcc tccgaaagag ggccaggtcc taagctgctg cttgtgcgcg 1260
 actgcaccgc gcattctctt cacctgaggc tttccgtccg ccagtgcagg aaccgggtgc 1320
 tcgctggg 1328

<210> 123
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 123

Met Asp Lys Leu Asp Ala Asn Val Ser Ser Glu Glu Gly Phe Gly Ser
1 5 10 15

Val Glu Lys Val Val Leu Leu Thr Phe Leu Ser Thr Val Ile Leu Met
20 25 30

Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Trp Asp Arg
35 40 45

Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala Phe
50 55 60

Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile Glu
65 70 75 80

Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val Arg
85 90 95

Thr Ser Leu Asp Val Leu Leu Thr Thr Ala Ser Ile Phe His Leu Cys
100 105 110

Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu Val
115 120 125

Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly
130 135 140

Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln Gly
 145 150 155 160
 Trp Asn Asn Ile Gly Ile Ile Asp Leu Ile Glu Lys Arg Lys Phe Asn
 165 170 175
 Gln Asn Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr
 180 185 190
 Ala Ile Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met
 195 200 205
 Val Leu Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His
 210 215 220
 Gln Ile Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro
 225 230 235 240
 Gln Ser Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys
 245 250 255
 Ala Ala Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp
 260 265 270
 Ala Pro Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr
 275 280 285
 Val Pro Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn
 290 295 300
 Ser Gly Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg
 305 310 315 320
 Arg Ala Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg
 325 330 335
 Pro Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn
 340 345 350
 Gly Ser Thr His Val Leu Arg Asp Ala Val Glu Cys Gly Gly Gln Trp
 355 360 365

Glu Ser Gln Cys His Pro Pro Ala Thr Ser Pro Leu Val Ala Ala Gln
 370 375 380

Pro Ser Asp Thr
 385

<210> 124
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 124

Met Asp Lys Leu Asp Ala Asn Val Ser Ser Glu Glu Gly Phe Gly Ser
 1 5 10 15

Val Glu Lys Val Val Leu Leu Thr Phe Leu Ser Thr Val Ile Leu Met
 20 25 30

Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Trp Asp Arg
 35 40 45

Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala Phe
 50 55 60

Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile Glu
 65 70 75 80

Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val Arg
 85 90 95

Thr Ser Leu Asp Val Leu Leu Thr Thr Ala Ser Ile Phe His Leu Cys
 100 105 110

Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu Val
 115 120 125

Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly
 130 135 140

Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln Gly
 145 150 155 160

Trp Asn Asn Ile Gly Ile Ile Asp Leu Ile Glu Lys Arg Lys Phe Asn

165 170 175
 Gln Asn Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr
 180 185 190
 Ala Ile Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met
 195 200 205
 Val Leu Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His
 210 215 220
 Gln Ile Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro
 225 230 235 240
 Gln Ser Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys
 245 250 255
 Ala Ala Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp
 260 265 270
 Ala Pro Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr
 275 280 285
 Val Pro Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn
 290 295 300
 Ser Gly Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg
 305 310 315 320
 Arg Ala Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg
 325 330 335
 Pro Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn
 340 345 350
 Gly Ser Thr His Val Leu Arg Asp Ala Val Glu Cys Gly Gly Gln Trp
 355 360 365
 Glu Ser Gln Cys His Pro Pro Ala Thr Ser Pro Leu Val Ala Ala Gln
 370 375 380
 Pro Ser Asp Thr

385

<210> 125
 <211> 2874
 <212> DNA
 <213> Homo sapiens

<400> 125
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 gggcgctgc tgcctgggac gctgagtcca caggttcaca ctctcaggcc agagaacctc 180
 ctgctggtgt ccaccttgga tggaaagtctc caogcactaa gcaagcagac aggggacctg 240
 aagtggactc tgagggatga tcccgctcgc gaaggaccaa tgtacgtcac agaaatggcc 300
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 acctaccgcc gctactcagc gccccccatg gatggctcac ccgggaaata catgagccac 660
 ctggcgctct gtgggatggg cctgctgctc actgtggacc cagaaagtgg ggcagtgctg 720
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 cgccagctgc cgcctctcac cctggctcga gacactctgc atttctctgc cctccgctgg 840
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 gggagtggaa ctgcagagac aagacccccca gagaacaccc agggcccagc cttcttcttg 1260
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 Ser Leu His Ala Leu Ser Lys Gln Thr Gly Asp Leu Lys Trp Thr Leu
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 Arg Asp Asp Pro Val Ile Glu Gly Pro Met Tyr Val Thr Glu Met Ala
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 Phe Leu Ser Asp Pro Ala Asp Gly Ser Leu Tyr Ile Leu Gly Thr Gln
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 Lys Gln Leu Gly Leu Met Lys Leu Pro Phe Thr Ile Pro Glu Leu Val
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 His Ala Ser Pro Cys Arg Ser Ser Asp Gly Val Phe Tyr Thr Gly Arg
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 Lys Gln Asp Ala Trp Phe Val Val Asp Pro Glu Ser Gly Glu Thr Gln
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 Arg Thr Gln Tyr Thr Val Thr Met His Asp Pro Arg Ala Pro Ala Leu
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 Arg Trp Asn Thr Thr Tyr Arg Arg Tyr Ser Ala Pro Pro Met Asp Gly
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 Ser Pro Gly Lys Tyr Met Ser His Leu Ala Ser Cys Gly Met Gly Leu
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 210 215 220

Leu Gly Met Pro Val Met Gly Val Tyr Thr Trp His Gln Asp Gly Leu
225 230 235 240

Arg Gln Leu Pro His Leu Thr Leu Ala Arg Asp Thr Leu His Phe Leu
245 250 255

Ala Leu Arg Trp Gly His Ile Arg Leu Pro Ala Ser Gly Pro Gln Asp
260 265 270

Thr Ala Thr Leu Phe Ser Ala Leu Asp Thr Gln Leu Leu Met Thr Leu
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Tyr Val Gly Lys Asp Glu Thr Gly Phe Tyr Val Ser Lys Ala Leu Val
290 295 300

His Thr Gly Val Ala Leu Val Pro Arg Gly Leu Thr Leu Ala Pro Thr
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Asp Gly Pro Thr Thr Asp Glu Val Thr Leu Gln Val Ser Gly Glu Arg
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Glu Gly Ser Pro Ser Thr Ala Val Arg Tyr Pro Ser Gly Ser Val Ala
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Leu Pro Ser Gln Trp Leu Leu Ile Gly His His Glu Leu Pro Pro Val
355 360 365

Leu His Thr Thr Met Leu Arg Val His Pro Thr Pro Gly Ser Gly Thr
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Ala Glu Thr Arg Pro Pro Glu Asn Thr Gln Ala Pro Ala Phe Phe Leu
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Glu Leu Leu Ser Leu Ser Arg Glu Lys Leu Trp Asp Ser Glu Leu His
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Pro Glu Glu Lys Ile Pro Asp Ser Tyr Leu Gly Leu Gly Pro Gln Asp
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 Asn Ile Leu Ile Thr Gly Pro Asp Thr Gln Gly Leu Gly Arg Val Val
 645 650 655
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 660 665 670

Phe Ser Leu His Ser Gly Ile Pro Gly Thr Glu Gly Trp Met Ala Pro
675 680 685

Glu Leu Leu Gln Leu Leu Pro Pro Asn Ser Pro Thr Ser Ala Val Asp
690 695 700

Ile Phe Ser Ala Gly Cys Val Phe Tyr Tyr Val Leu Ser Gly Gly Ser
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His Pro Phe Gly Asp Ser Leu Tyr Arg Gln Ala Asn Ile Leu Thr Gly
725 730 735

Val Pro Cys Leu Ala His Leu Glu Glu Glu Val His Asp Lys Val Val
740 745 750

Ala Arg Asp Leu Val Ala Ala Met Leu Ser Leu Leu Pro Gln Ala Arg
755 760 765

Pro Ser Ala Pro Gln Val Leu Ala His Pro Phe Phe Trp Ser Arg Ala
770 775 780

Lys Gln Leu Gln Phe Phe Gln Asp Val Ser Asp Trp Leu Glu Lys Glu
785 790 795 800

Ser Glu Gln Glu Pro Leu Met Arg Ala Leu Glu Ala Gly Gly Cys Thr
805 810 815

Val Val Arg Asp Asn Trp His Glu His Ile Ser Met Pro Leu Gln Ile
820 825 830

Asp Leu Arg Lys Phe Arg Ser Tyr Lys Gly Thr Ser Val Arg Asp Leu
835 840 845

Leu Arg Ala Val Arg Asn Lys Lys His His Tyr Arg Glu Leu Pro Val
850 855 860

Glu Val Arg Gln Ala Leu Gly Gln Val Pro Asp Gly Phe Val Gln Tyr
865 870 875 880

Phe Thr Asn Arg Phe Pro Gln Leu Leu Leu His Thr His Arg Val Met
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Ile Asn Ser Thr Gly Ser Thr Arg Gly His Ala Ser Thr Ser Ser Tyr
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Arg Arg Ala His Ser Pro Ala Ser Thr Leu Pro Asn Ser Pro Gly Ser
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Thr Phe Glu Arg Lys Thr His Val Thr Arg His Ala Tyr Glu Gly Ser
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Ser Ser Thr Arg Gly Arg Ser Gln Thr Arg Glu Ser Glu Ile Arg Val
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Arg Leu Gln Ser Ala Ser Pro Ser Thr Arg Trp Thr Glu Leu Asp Asp
145 150 155 160

Val Lys Arg Leu Leu Lys Gly Ser Arg Ser Ala Ser Val Ser Pro Thr
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Arg Asn Ser Ser Asn Thr Leu Pro Ile Pro Lys Lys Gly Thr Val Glu
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Thr Lys Ile Val Thr Ala Ser Ser Gln Ser Val Ser Gly Thr Tyr Asp
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Ala Thr Ile Leu Asp Ala Asn Leu Pro Ser His Val Trp Ser Ser Thr
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Leu Pro Ala Gly Ser Ser Met Gly Thr Tyr His Asn Asn Met Thr Thr
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Gln Ser Ser Ser Leu Leu Asn Thr Asn Ala Tyr Ser Ala Gly Ser Val
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Phe Gly Val Pro Asn Asn Met Ala Ser Cys Ser Pro Thr Leu His Pro
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Pro Gly Pro Leu Gly His Pro Gly Pro Gln Gly Pro Lys Gly Gln Lys
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Pro Arg Gly Glu Gln Gly Leu Thr Gly Met Pro Gly Ile Arg Gly Pro
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Ser Ile Gly Leu Pro Gly Pro Pro Gly Pro Pro Gly Leu Pro Gly
 1145 1150 1155

Thr Ser Tyr Glu Glu Leu Leu Ser Leu Leu Arg Gly Ser Glu Phe
 1160 1165 1170

Arg	Gly	Ile	Val	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Ile
1175						1180					1185			
Pro	Gly	Asn	Val	Trp	Ser	Ser	Ile	Ser	Val	Glu	Asp	Leu	Ser	Ser
1190						1195					1200			
Tyr	Leu	His	Thr	Ala	Gly	Leu	Ser	Phe	Ile	Pro	Gly	Pro	Pro	Gly
1205						1210					1215			
Pro	Pro	Gly	Pro	Pro	Gly	Pro	Arg	Gly	Pro	Pro	Gly	Val	Ser	Gly
1220						1225					1230			
Ala	Leu	Ala	Thr	Tyr	Ala	Ala	Glu	Asn	Ser	Asp	Ser	Phe	Arg	Ser
1235						1240					1245			
Glu	Leu	Ile	Ser	Tyr	Leu	Thr	Ser	Pro	Asp	Val	Arg	Ser	Phe	Ile
1250						1255					1260			
Val	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Gln	Gly	Pro	Pro	Gly	Asp
1265						1270					1275			
Ser	Arg	Leu	Leu	Ser	Thr	Asp	Ala	Ser	His	Ser	Arg	Gly	Ser	Ser
1280						1285					1290			
Ser	Ser	Ser	His	Ser	Ser	Ser	Val	Arg	Arg	Gly	Ser	Ser	Tyr	Ser
1295						1300					1305			
Ser	Ser	Met	Ser	Thr	Gly	Gly	Gly	Gly	Ala	Gly	Ser	Leu	Gly	Ala
1310						1315					1320			
Gly	Gly	Ala	Phe	Gly	Glu	Ala	Ala	Gly	Asp	Arg	Gly	Pro	Tyr	Gly
1325						1330					1335			
Thr	Asp	Ile	Gly	Pro	Gly	Gly	Gly	Tyr	Gly	Ala	Ala	Ala	Glu	Gly
1340						1345					1350			
Gly	Met	Tyr	Ala	Gly	Asn	Gly	Gly	Leu	Leu	Gly	Ala	Asp	Phe	Ala
1355						1360					1365			
Gly	Asp	Leu	Asp	Tyr	Asn	Glu	Leu	Ala	Val	Arg	Val	Ser	Glu	Ser
1370						1375					1380			

Met Gln Arg Gln Gly Leu Leu Gln Gly Met Ala Tyr Thr Val Gln
1385 1390 1395

Gly Pro Pro Gly Gln Pro Gly Pro Gln Gly Pro Pro Gly Ile Ser
1400 1405 1410

Lys Val Phe Ser Ala Tyr Ser Asn Val Thr Ala Asp Leu Met Asp
1415 1420 1425

Phe Phe Gln Thr Tyr Gly Ala Ile Gln Gly Pro Pro Gly Gln Lys
1430 1435 1440

Gly Glu Met Gly Thr Pro Gly Pro Lys Gly Asp Arg Gly Pro Ala
1445 1450 1455

Gly Pro Pro Gly His Pro Gly Pro Pro Gly Pro Arg Gly His Lys
1460 1465 1470

Gly Glu Lys Gly Asp Lys Gly Asp Gln Val Tyr Ala Gly Arg Arg
1475 1480 1485

Arg Arg Arg Ser Ile Ala Val Lys Pro
1490 1495

<210> 129
<211> 460
<212> DNA
<213> Homo sapiens

<220>
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<223> n = unknown

<400> 129
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 agccttcccc tcacaccttc aaatgccctt cagtgatctg tagaacaact cggggcatat 180
 tcaagaaggg caaaacttca tgcctcttgc cctcaatcc tcttttccct ttggtttgggt 240
 ttctttactt cttgccaaaa aacagctacc ttggcgaggg aagttattac aatccattgc 300
 aagtacttcc tccaataatg aacacaaçaa aatcctttct ttattcattt aaagcacgaa 360

gctggccctc tttaaaata ccctgttttt aataaatcct cggtaataga catccattca 420
 cgagaataaa gtgggtacat tggagctgaa gctgggtgta 460

<210> 130
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 130

Met Pro Leu Ala Pro Gln Ser Ser Phe Pro Phe Gly Leu Val Ser Leu
 1 5 10 15

Leu Leu Ala Lys Lys Gln Leu Pro Leu Ala Gly Lys Leu Leu Gln Ser
 20 25 30

Ile Ala Ser Thr Ser Ser Asn Asn Glu His Asn Lys Ile Leu Ser Leu
 35 40 45

Phe Ile
 50

<210> 131
 <211> 1017
 <212> DNA
 <213> Homo sapiens

<400> 131

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 ctactaagag caaggatgcc cagctctgtg gccggtgctg tgccgagttc tttgaattat 180
 cagatcttct gctccacaag aagaactgta ctaaaaatca attagtttta atcgtaaattg 240
 aaaatccagc ctccccacc gaaaccttct cccccagccc cctcctgat aatcctgatg 300
 aacaaatgaa tgacacagtt aacaaaacag atcaagtgga ctgcagcgac ctttcagaac 360
 acaacggact tgacagggaa gagtccatgg aggtggaggc cccggttgct aacaaaagcg 420
 gcagcggcac ttccagcggc agccacagca gtaccgcccc aagcagcagc agcagcagca 480
 gcagcagcag cggcggcggc ggcagctcct ccacaggtac ctacgcgac acaacctctc 540
 tacctcaact cggggacctg acaacactgg gcaacttctc cgtaatcaac agcaacgtca 600
 tcacgcagaa cctccagagc accaaggtgg cgggtggcca gttctcccag gaagcgaggt 660

gcggcggggc ctctgggggc aagctggcgc tcccagccct catggaacaa ctcttagctc 720
 tgcagcagca gcagatccac cagctgcaat tgatcgaaca gattcgtcac caaatattgc 780
 tgttggttc tcagaatgca gacttgccaa catcttctag tccttctcaa ggtactttac 840
 gaacatctgc caaacccctt gtcccacgct aagttcccat ttatctcagc agctgggcag 900
 caacaagctt ggattggggc cagaagccct cgccagccca ttctgccaag aattaattgg 960
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<210> 132
 <211> 285
 <212> PRT
 <213> Homo sapiens

<400> 132

Met Ser Arg Arg Lys Gln Ala Lys Pro Gln His Phe Gln Ser Asp Pro
 1 5 10 15

Glu Val Ala Ser Leu Pro Arg Arg Asp Gly Asp Thr Glu Lys Gly Gln
 20 25 30

Pro Ser Arg Pro Thr Lys Ser Lys Asp Ala His Val Cys Gly Arg Cys
 35 40 45

Cys Ala Glu Phe Phe Glu Leu Ser Asp Leu Leu Leu His Lys Lys Asn
 50 55 60

Cys Thr Lys Asn Gln Leu Val Leu Ile Val Asn Glu Asn Pro Ala Ser
 65 70 75 80

Pro Pro Glu Thr Phe Ser Pro Ser Pro Pro Pro Asp Asn Pro Asp Glu
 85 90 95

Gln Met Asn Asp Thr Val Asn Lys Thr Asp Gln Val Asp Cys Ser Asp
 100 105 110

Leu Ser Glu His Asn Gly Leu Asp Arg Glu Glu Ser Met Glu Val Glu
 115 120 125

Ala Pro Val Ala Asn Lys Ser Gly Ser Gly Thr Ser Ser Gly Ser His
 130 135 140

Ser Ser Thr Ala Pro Ser Ser Ser Ser Ser Ser Ser Ser Ser Gly
145 150 155 160

Gly Gly Gly Ser Ser Ser Thr Gly Thr Ser Ala Ile Thr Thr Ser Leu
165 170 175

Pro Gln Leu Gly Asp Leu Thr Thr Leu Gly Asn Phe Ser Val Ile Asn
180 185 190

Ser Asn Val Ile Ile Glu Asn Leu Gln Ser Thr Lys Val Ala Val Ala
195 200 205

Gln Phe Ser Gln Glu Ala Arg Cys Gly Gly Ala Ser Gly Gly Lys Leu
210 215 220

Ala Val Pro Ala Leu Met Glu Gln Leu Leu Ala Leu Gln Gln Gln Gln
225 230 235 240

Ile His Gln Leu Gln Leu Ile Glu Gln Ile Arg His Gln Ile Leu Leu
245 250 255

Leu Ala Ser Gln Asn Ala Asp Leu Pro Thr Ser Ser Ser Pro Ser Gln
260 265 270

Gly Thr Leu Arg Thr Ser Ala Lys Pro Leu Val Pro Arg
275 280 285

<210> 133
<211> 482
<212> DNA
<213> Homo sapiens

<220>
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<222> (476)..(476)
<223> n = unknown

<400> 133
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cgctccgctc gctgcttcag ccgccgcccc ctgcagcatc ttctacgtcg ggaccacagc 180
ctccgcctcc acaaagcctg aacctccttt cgcaggctca gctgcaggca cagctcattg 240

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cgccaggcgg aactcaaatg aaaaagaaaa gtggcttcca gataactagc gttactcctg    300
ctcagatctc cgctagtatc agctctaaca acagtatagc agaggacact gagagctatg    360
atgatctgga tgaatctcac acggaagatc tctcttcttc ggagatcctt gatgtgtcac    420
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ct                                                                    482

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<210> 134
<211> 158
<212> PRT
<213> Homo sapiens

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<220>
<221> MISC FEATURE
<222> (156)..(156)
<223> X = unknown

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<400> 134

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Met Ala His Pro Ala Met Phe Pro Arg Arg Gly Ser Gly Ser Gly Ser
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Ala Ser Ala Leu Asn Ala Ala Gly Thr Gly Val Gly Ser Asn Ala Thr
20          25          30

```

```

Ser Ser Glu Asp Phe Pro Pro Pro Ser Leu Leu Gln Pro Pro Pro Pro
35          40          45

```

```

Ala Ala Ser Ser Thr Ser Gly Pro Gln Pro Pro Pro Pro Gln Ser Leu
50          55          60

```

```

Asn Leu Leu Ser Gln Ala Gln Leu Gln Ala Gln Leu Ile Ala Pro Gly
65          70          75          80

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```

Gly Thr Gln Met Lys Lys Lys Ser Gly Phe Gln Ile Thr Ser Val Thr
85          90          95

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Pro Ala Gln Ile Ser Ala Ser Ile Ser Ser Asn Asn Ser Ile Ala Glu
100         105         110

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```

Asp Thr Glu Ser Tyr Asp Asp Leu Asp Glu Ser His Thr Glu Asp Leu
115         120         125

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Ser Ser Ser Glu Ile Leu Asp Val Ser Leu Ser Arg Ala Thr Asp Leu
 130 135 140

Gly Glu Pro Glu Arg Ser Ser Ser Glu Glu Thr Xaa Ile Thr
 145 150 155

<210> 135
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 135
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 taactaatgc atagcattct atccaatgga tgccctatag ttttttatcc aggccatatt 180
 gaccgacatt taagcaattt caaatctttt actattgcaa acaatgctgc aactcagctt 240
 tttacatgcg cttttctgca catgggcaaa cattcctcta gaaagcaaga aataaaattg 300
 ctgggttgaa agatgtgtgc attttcagtg ttaataatgt caaattagcc tctaacaaga 360
 tggtgcctat ttcatttact atcagaaatg g 391

<210> 136
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 136

Met His Ser Ile Leu Ser Asn Gly Cys Pro Ile Val Phe Tyr Pro Gly
 1 5 10 15

His Ile Asp Arg His Leu Ser Asn Phe Lys Ser Phe Thr Ile Ala Asn
 20 25 30

Asn Ala Ala Thr Gln Leu Phe Thr Cys Ala Phe Leu His Met Gly Lys
 35 40 45

His Ser Ser Arg Lys Gln Glu Ile Lys Leu Leu Gly
 50 55 60

<210> 137
 <211> 396
 <212> DNA
 <213> Homo sapiens

<400> 137
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 gagaaacagt ctttgtatta caatacagtt cagatatgta ttaatcatgc tacacaacag 120
 gggcagagtg cacattaataa tccaaagggt agcccagctt ttatttcaac caatatcttt 180
 cttccttttt ctctagcaaa cgatttcaca gtatttccta aaaacagaag aaccacatc 240
 tgaaacattg gtagtttggg gtgcatcaca agctctcata ttagaaaaga aactgtaata 300
 tgttacaggc catgaggctg tagtgattct cagtgtgctg tactgttaaa aggtagatct 360
 ccaaaataat aaaaagaggt gcgttatttg ttggag 396

<210> 138
 <211> 3254
 <212> DNA
 <213> Homo sapiens

<400> 138
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 ccagctgta gcggacaggt gcagcctggc atgggggagc gtggaggcgg gcccggtggc 180
 ggctccgggg acctcatctt ccaagatgga cacctcatct ctgggtccct ggaggccctg 240
 atggagcacc ttgttccac ggtggactat taccgcgata ggacgtacat cttcaccttt 300
 ctctgagct cccgggtctt tatgccccct catgacctgc tggcccgct ggggcagatc 360
 tgcgtggagc agaagcagca gctggaagcc gggcctgaaa aggccaaagt gaagtctttc 420
 tcagccaaga tcgtgcagct cctgaaggag tggaccgagg ccttccccta tgacttccag 480
 gatgagaagg ccatggccga gctgaaagcc atcacacacc gtgtcaccca gtgtgatgag 540
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 gggcccatcc tcaagaccaa gccaccagcc gccagaagg acatcctggg cgtgtgctgc 720
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 taccctgagg acttgatgca gatcgtcagc cacatggact cattggacaa ccacaggtgc 840
 cgaggggacc tgaccaagac ctacagcctg gaggcctatg acaactgggt caactgcctg 900
 agcatgctgg tggccactga ggtgtgccgg gtggtgaaga agaaacaccg gaccgcgatg 960
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atggccatca tctctggcat gaacctcagt cctgtggcaa ggctgaagaa aacttggtcc	1080
aaggtcaaga cagccaagtt tgatgtcttg gagcatcaca tggacccgtc cagcaacttc	1140
tgcaactacc gtacagccct gcagggggcc acgcagaggt cccagatggc caacagcagc	1200
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aaaattcgcc aggcatact gctggagccc attcagataa aactgcccaa atactgagag	2520
gtgttttcta caccagcta gaggagcaca ctccattttc ccatgtctga cttcgtggtg	2580
tgagccctgg gccctactga ccatggcgca ggacagctgt ccttcagaaa gcacacggtc	2640
aatccacgtg gaccgtctcc ctgcaggaa ctccgcaccc ttgtccctct ctgcattccc	2700

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gccctgggcc cgttgcccat gcctctggtc ctgggtggag caggaatagt tccactgtat 2880
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aaaaaaaaa aaaa 3254

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<210> 139
 <211> 428
 <212> PRT
 <213> Homo sapiens

<400> 139

Met Glu His Leu Val Pro Thr Val Asp Tyr Tyr Pro Asp Arg Thr Tyr
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Ile Phe Thr Phe Leu Leu Ser Ser Arg Val Phe Met Pro Pro His Asp
 20 25 30

Leu Leu Ala Arg Val Gly Gln Ile Cys Val Glu Gln Lys Gln Gln Leu
 35 40 45

Glu Ala Gly Pro Glu Lys Ala Lys Leu Lys Ser Phe Ser Ala Lys Ile
 50 55 60

Val Gln Leu Leu Lys Glu Trp Thr Glu Ala Phe Pro Tyr Asp Phe Gln
 65 70 75 80

Asp Glu Lys Ala Met Ala Glu Leu Lys Ala Ile Thr His Arg Val Thr
 85 90 95

Gln Cys Asp Glu Glu Asn Gly Thr Val Lys Lys Ala Ile Ala Gln Met
 100 105 110

Thr Gln Ser Leu Leu Leu Ser Leu Ala Ala Arg Ser Gln Leu Gln Glu
 115 120 125
 Leu Arg Glu Lys Leu Arg Pro Pro Ala Val Asp Lys Gly Pro Ile Leu
 130 135 140
 Lys Thr Lys Pro Pro Ala Ala Gln Lys Asp Ile Leu Gly Val Cys Cys
 145 150 155 160
 Asp Pro Leu Val Leu Ala Gln Gln Leu Thr His Ile Glu Leu Asp Arg
 165 170 175
 Val Ser Ser Ile Tyr Pro Glu Asp Leu Met Gln Ile Val Ser His Met
 180 185 190
 Asp Ser Leu Asp Asn His Arg Cys Arg Gly Asp Leu Thr Lys Thr Tyr
 195 200 205
 Ser Leu Glu Ala Tyr Asp Asn Trp Phe Asn Cys Leu Ser Met Leu Val
 210 215 220
 Ala Thr Glu Val Cys Arg Val Val Lys Lys Lys His Arg Thr Arg Met
 225 230 235 240
 Leu Glu Phe Phe Ile Asp Val Ala Arg Glu Cys Phe Asn Ile Gly Asn
 245 250 255
 Phe Asn Ser Met Met Ala Ile Ile Ser Gly Met Asn Leu Ser Pro Val
 260 265 270
 Ala Arg Leu Lys Lys Thr Trp Ser Lys Val Lys Thr Ala Lys Phe Asp
 275 280 285
 Val Leu Glu His His Met Asp Pro Ser Ser Asn Phe Cys Asn Tyr Arg
 290 295 300
 Thr Ala Leu Gln Gly Ala Thr Gln Arg Ser Gln Met Ala Asn Ser Ser
 305 310 315 320
 Arg Glu Lys Ile Val Ile Pro Val Phe Asn Leu Phe Val Lys Asp Ile
 325 330 335

Tyr Phe Leu His Lys Ile His Thr Asn His Leu Pro Asn Gly His Ile
 340 345 350

Asn Phe Lys Lys Phe Trp Glu Ile Ser Arg Gln Ile His Glu Phe Met
 355 360 365

Thr Trp Thr Gln Val Glu Cys Pro Phe Glu Lys Asp Lys Lys Ile Gln
 370 375 380

Ser Tyr Leu Leu Thr Ala Pro Ile Tyr Ser Glu Glu Ala Leu Phe Val
 385 390 395 400

Ala Ser Phe Glu Ser Glu Gly Pro Glu Asn His Val Glu Lys Asp Ser
 405 410 415

Trp Lys Thr Leu Arg Thr Thr Leu Leu Asn Arg Ala
 420 425

<210> 140
 <211> 495
 <212> DNA
 <213> Homo sapiens

<400> 140
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 ccaagaatct atcccaatga ggtagttaca taaatatgca agtatacaca agatgtttcat 180
 cacaattaga aacaacccaaa atgtccacca acatgagact agttcaaaaa gatacgaggt 240
 attcatacaa gagacttttat gcatccactg aaaagaatca tgtaattcat attgggttgac 300
 tcaaatagaa gtcctcatcac atatttttaa gacaaaagga attacaaagc agtatgggtg 360
 acataatccc atttatgtgc aaatcaaata aattccagat ttactgtgg ttcaattcag 420
 cccagtgtca cattcacaga aacaaccag caacaaaaag gcattacaga gtaatttcag 480
 ccttggtctt ccatt 495

<210> 141
 <211> 45
 <212> PRT
 <213> Homo sapiens

<400> 141

Met Gln Val Tyr Thr Arg Cys Ser Ser Gln Leu Glu Thr Thr Lys Met
1 5 10 15

Ser Thr Asn Met Arg Leu Val Gln Lys Asp Thr Arg Tyr Ser Tyr Lys
20 25 30

Arg Leu Tyr Ala Ser Thr Glu Lys Asn His Val Ile His
35 40 45

<210> 142
<211> 470
<212> DNA
<213> Homo sapiens

<400> 142
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gaagtgtctt aactgaagtg agcacaggaa attggacctt tttgtttgat cctgagatct 180
ggacagaagg caatcctcct ccttccttca gaggatacaa tggagaccca gagcaatctg 240
ctcagcacca gtaagctgga agccatgctg ccttcacccc aattctctgt ggggatgctg 300
tgctggtttc agtccttggg tctgtctcct agttcagcct ctcttgcttg cttctcagat 360
gtgtctggtg gtagaagttg aggaagagaa cgaggaggct gagggcttac aggagcacag 420
atgtgttgaa cccaacaggg aaggggcact cagtgaggag actgtaggaa 470

<210> 143
<211> 97
<212> PRT
<213> Homo sapiens

<400> 143

Leu Asp Arg Arg Gln Ser Ser Ser Phe Leu Gln Arg Ile Gln Trp Arg
1 5 10 15

Pro Arg Ala Ile Cys Ser Ala Pro Val Ser Trp Lys Pro Cys Cys Leu
20 25 30

Pro Pro Asn Ser Leu Trp Gly Cys Cys Ala Gly Phe Ser Pro Trp Val
35 40 45

Leu Leu Leu Val Gln Pro Leu Leu Leu Ala Ser Gln Met Cys Leu Val
50 55 60

Val Glu Val Glu Glu Glu Asn Glu Glu Ala Glu Gly Leu Gln Glu His
65 70 75 80

Arg Cys Val Glu Pro Asn Arg Glu Gly Ala Leu Ser Glu Glu Thr Val
85 90 95

Gly

<210> 144
<211> 449
<212> DNA
<213> Homo sapiens

<400> 144
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tgaataaatt ttttaaaacg atcttcatat gttatTTttc atttgcagcc agaggaaaaa 120
aacttgtaac tttctgtgga actttccaga caattttaca gatatggacc atttttaaca 180
gatcttttaa cctatacaCT ttttaataag ccaaacagga acggggagaac atcatttcag 240
tgaaacaaac agatggaaac attgtgaatg tcagaaccac agtcaggaat gttccttttt 300
tctcatcttc ccttattgtc aggttttatt gttttcttga aatgttatct cagtctttta 360
atggcttctc tctacactga gtgaaaatgt gctggccgat tcgcatcttt gtcaccactc 420
ggtgtactcg agataaatgt ataaatagg 449

<210> 145
<211> 30
<212> PRT
<213> Homo sapiens

<400> 145

Met Ser Glu Pro Gln Ser Gly Met Phe Leu Phe Ser His Leu Pro Leu
1 5 10 15

Leu Ser Gly Phe Ile Val Phe Leu Lys Cys Tyr Leu Ser Leu
20 25 30

<210> 146
<211> 423
<212> DNA
<213> Homo sapiens

<400> 146
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 gagccccctt cccaatcctg gagctgtata cgccaccggg aagggccgcg gaattggaga 180
 ggtgctgcag aggggtctata cctcttgctg tttcccggt ctgctcatct tccccaaactg 240
 cccttaaggc gcctccgtgg gcgcgctgat taggctctcg gatgttggtg ggaagatcga 300
 aacgaagggc taagcccccc tcgcccgggt cctgccggaa agttcagctc ggcggectcc 360
 aggatcaaaa attttaaagg ctgcagcccg gtccccagtg gatcggccag ataacaagaa 420
 act 423

<210> 147
 <211> 88
 <212> PRT
 <213> Homo sapiens

<400> 147

Leu Ser Lys Gln Gly Leu Leu Thr Gly Val Ser Arg Gln Arg Ile Ala
 1 5 10 15

Thr Pro Ala Ala Arg Gly Arg Ala Cys Gly Arg Gly Arg Gly Ala Gly
 20 25 30

Arg Pro Ala Gly Arg Ala Thr Gly Ala Pro Phe Pro Ile Leu Glu Leu
 35 40 45

Tyr Thr Pro Pro Gly Arg Ala Ala Glu Leu Glu Arg Cys Cys Arg Gly
 50 55 60

Ser Ile Pro Leu Ala Val Ser Arg Leu Cys Ser Ser Ser Pro Thr Ala
 65 70 75 80

Leu Lys Ala Pro Pro Trp Ala Arg
 85

<210> 148
 <211> 661
 <212> DNA
 <213> Homo sapiens

<400> 148
 aaaaagcata ctgaaagcat ttcataaacg atagcactcc gtataaagta tgatcaccaa 60

gagggcagct tattcttgct taggactaag tagaaataac attcattcaa gattaactct 120
 gtcttcctgt ctctgaagag tgttgggaca gggagagccg ccttttccag ggtttgcaaa 180
 acaagctaca tgttgggacc accaatggag cccgtctccc tgggctttca gcttcccctc 240
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 tgagaagccc tgcagggcag tctcaccagc ccaggggtggc cctgcccagc cctggtcagt 360
 gaagaggagc ttccagacac acccatcctg atgttggtgcc catcttccct gaatgcactg 420
 agggcggaag ggcctagctg gagactgcca tcacgtagtt cttggagggg ctgctccggc 480
 ccagcagcac ttggttcttg caggtgagga gccacagga ggcggccagt ggggcctcct 540
 cgtacaagac gcagaatgag ccgtcctact caatgcggta ggacacctca taggggtcca 600
 cccacagggg cagctcgcat ggcagcagct ggtgcagctg aggctggctg agtacgatct 660
 g 661

<210> 149
 <211> 38
 <212> PRT
 <213> Homo sapiens

<400> 149

Met Leu Cys Pro Ser Ser Leu Asn Ala Leu Arg Ala Glu Gly Pro Ser
 1 5 10 15

Trp Arg Leu Pro Ser Arg Ser Ser Trp Arg Gly Cys Ser Gly Pro Ala
 20 25 30

Ala Leu Gly Ser Cys Arg
 35

<210> 150
 <211> 502
 <212> DNA
 <213> Homo sapiens

<400> 150

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 gtgaacgccc tccctcaggg ctggccgggt gcgtctgggg ttgtcctagc tccagctgct 180
 ggaacaaaat accgagcctg gggacttaag caacagaaat gtattttctc acagcctcgg 240

```

aggggggaggg gaaggtccgg tgtcccaggg ttgccgggct ggttctgcgg aggcctctcc 300
cgctgctgcc ttctctcagg cggcctctgc gcaggtccgt cccgtgtccc tctgccctaa 360
cctcctcctg caactaggac accagtggga cccggccagg gctcatcctc acggctgctt 420
cacacatact cacctgtctc gtagccccctt ctccacacac gctcgcgttg ttggtactga 480
gagtttggat tctaaccatg aa 502

```

```

<210> 151
<211> 119
<212> PRT
<213> Homo sapiens

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<400> 151

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```

Ala Ala Ala Trp Ala Pro Gly Cys Leu Gln Gly Ile Tyr Thr Gly Leu
1          5          10          15

```

```

Ser Gly Thr Thr Arg Val Pro Arg Ala Glu Glu Gly Ala His Ala Ala
          20          25          30

```

```

Ser Tyr Asn Ala Tyr Gly Lys Pro Val Asn Ala Leu Pro Gln Gly Trp
          35          40          45

```

```

Pro Gly Ala Ser Gly Val Val Leu Ala Pro Ala Ala Gly Thr Lys Tyr
          50          55          60

```

```

Arg Ala Trp Gly Leu Lys Gln Gln Lys Cys Ile Phe Ser Gln Pro Arg
          65          70          75          80

```

```

Arg Gly Arg Gly Arg Ser Gly Val Pro Gly Leu Pro Gly Trp Phe Cys
          85          90          95

```

```

Gly Gly Leu Ser Arg Cys Cys Leu Leu Ser Gly Gly Leu Cys Ala Gly
          100          105          110

```

```

Pro Ser Arg Val Pro Leu Pro
          115

```

```

<210> 152
<211> 109
<212> PRT
<213> Homo sapiens

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```

<400> 152

```

Leu Leu Glu Gln Asn Thr Glu Pro Gly Asp Leu Ser Asn Arg Asn Val
 1 5 10 15

Phe Ser His Ser Leu Gly Gly Gly Gly Glu Gly Pro Val Ser Gln Gly
 20 25 30

Cys Arg Ala Gly Ser Ala Glu Ala Ser Pro Ala Ala Ala Phe Ser Gln
 35 40 45

Ala Ala Ser Ala Gln Val Arg Pro Val Ser Leu Cys Pro Asn Leu Leu
 50 55 60

Leu Gln Leu Gly His Gln Trp Asp Pro Ala Arg Ala His Pro His Gly
 65 70 75 80

Cys Phe Thr His Thr His Leu Ser Arg Ser Pro Phe Ser Thr His Ala
 85 90 95

Arg Val Val Gly Thr Glu Ser Leu Asp Ser Asn His Glu
 100 105

<210> 153

<211> 624

<212> DNA

<213> Homo sapiens

<400> 153

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gcctgctgat gcaggctgca cagaggacat tgattagcac agcaagaagc attatcaatt      180
tcagcttttag tagaatgagg actcaagaca cttgtgaaac aaaatgaagg caaagtcccta      240
tattttgaca cttttctctc cctcccaaac attcacgggt gctttaccca cacctaattc      300
cacagcattt ttttctttaa taacacgtct tttatcaggt ctttcccaag ttttcaactt      360
tttttcatag agattactct cttcacactc ataattgttt gatttttggt atattgaatt      420
aaattacatc gttattaagt acaacttgca aaaacaagtt ttggaacaaa tacaactgat      480
tttttttttt ttttttgaga tggagtcttg ctctgtcttc aaataaaaat aaataaataa      540
aactctccaa gagcacccat ttgctagaca ctatgggggg actatcctgt ctactggtgc      600
cctcttgtgt taaaacagca ggtc                                             624

```

<210> 154
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 154

Met Lys Ala Lys Ser Tyr Ile Leu Thr Leu Phe Ser Pro Ser Gln Thr
 1 5 10 15

Phe Thr Val Ala Leu Pro Thr Pro Asn Ser Thr Ala Phe Phe Ser Leu
 20 25 30

Ile Thr Arg Leu Leu Ser Gly Leu Ser Gln Val Phe Asn Met Lys Ala
 35 40 45

Lys Ser Tyr Ile Leu Thr Leu Phe Ser Pro Ser Gln Thr Phe Thr Val
 50 55 60

Ala Leu Pro Thr Pro Asn Ser Thr Ala Phe Phe Ser Leu Ile Thr Arg
 65 70 75 80

Leu Leu Ser Gly Leu Ser Gln Val Phe Asn
 85 90

<210> 155
 <211> 304
 <212> DNA
 <213> Homo sapiens

<400> 155

gaaagggtaa aacaaaaaat ccacatcctc tccccaaccc cagcttctgg gcggaaatac 60
 gggctttcac ttttaaccct gactggctct ggctccaggg cctgagatgc cttcataatc 120
 tagtaactgg gtcccgggca tcctcgcgaa accgctgggt cactgccttg ctggcagctt 180
 cgggggatcg ctgggtcccc gacttggttg cagcctggag agactgctgg gtcccggcct 240
 cctgcacctc caccggagaa ccctgtgtcc cgacctcctg gacttccacc gaacgctggg 300
 tccc 304

<210> 156
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 156

Leu Arg Cys Leu His Asn Leu Val Thr Gly Ser Arg Ala Ser Ser Arg
1 5 10 15

Asn Arg Trp Val Thr Ala Leu Leu Ala Ala Ser Gly Asp Arg Trp Val
20 25 30

Pro Asp Leu Leu Ala Ala Trp Arg Asp Cys Trp Val Pro Ala Ser Cys
35 40 45

Thr Ser Thr Gly Glu Pro Cys Val Pro Thr Ser Trp Thr Ser Thr Glu
50 55 60

Arg Trp Val
65

<210> 157
<211> 262
<212> DNA
<213> Homo sapiens

<400> 157
tctcaaacat atttgatgtt tattactgta tcaactttgaa tatttgcgag agcctattta 60
cttctagcag aggtttacat tagcaatata aagtaataaa taaataaata aataaataaa 120
taaataaatg aagtccgggt ttttcttttc agtgtgggag accccacata aagcaacaat 180
gtatcatagc ttgacactg gataaatggg atgttaagag tgcacttcta ttcaataaca 240
tgcaaatggt gacataattc ac 262

<210> 158
<211> 483
<212> DNA
<213> Homo sapiens

<400> 158
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ccagcggctc ctcttttgag gagctggacc tggagggtga ggggcccttg gaggaaccac 120
ggctggaccc tgagactgag cccctggggg ctaccaagtg gccctgagag ccagtaacc 180
tgagaagggc aaggagtaac ccatgaccag cccctcctg cggggcaggg ctgcggaacc 240
gagcagactc tccagccatc ttcctccttc ttctgggggc gaggggttcc caggggacgt 300
aactccccct gctctaggcc tcttgtgaag ccttctcctc actgtccttt aggctcccag 360
ggccaaagca gccaaagact gtatcctgca ccagccctgt gggccgacac tctgtgtat 420

ctctcttcag actgtcactg agcttccaga cccagaataa accaatgact tacttgttca 480
 aaa 483

<210> 159
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 159

Met Val Thr Pro Ala Val Ser Ala Ala Ala Glu Ser Gln Val Pro Ala
 1 5 10 15

Ala Pro Leu Leu Arg Ser Trp Thr Trp Arg Val Arg Gly Pro Trp Arg
 20 25 30

Asn His Gly Trp Thr Leu Arg Leu Ser Pro Trp Gly Leu Pro Ser Gly
 35 40 45

Pro Glu Ser Pro Val Pro
 50

<210> 160
 <211> 576
 <212> DNA
 <213> Homo sapiens

<400> 160

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 cttggtgaat ttgttatatg tctataccca ccacgggtctc catcaaaaata ttttatcgtc 120
 ccagaaattt ccttggggcc ccacctcctc ctcaaagggtt atcactattc tgatgtctat 180
 caccatagat ttgtttttcc tgttcatgta aatggaacca taaacagccc tcttgtgtct 240
 gttttcttca cttaatatag tgtcattgag atttatctat gttgtattat cagtagttta 300
 tgcttttttaa ttgctgggta tagtccatag tctgaatata ccacaattta aaaattctat 360
 tctgtttaca aacatttgag ttctgtcctc cagggttcctc catgttatca caaatgacag 420
 aatttccttc ctcatcaagg ctgaatagta ttccattgtg tagatatacc acattttctt 480
 tatccattca tccacgatg gacagttagg ttgattccat atcttggcta ttgtgaataa 540
 tctgcatgt tttattgtta tgaataaagc tgctgt 576

<210> 161

<211> 30
 <212> PRT
 <213> Homo sapiens

<400> 161

Met Leu Ser Gln Met Thr Glu Phe Pro Ser Ser Ser Arg Leu Asn Ser
 1 5 10 15

Ile Pro Leu Cys Arg Tyr Thr Thr Phe Ser Leu Ser Ile His
 20 25 30

<210> 162
 <211> 500
 <212> DNA
 <213> Homo sapiens

<400> 162
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 ttatgcgtga ggagctggca ctgcgtatcg ggctgaccga gtcccagtg caggctgcct 180
 gtgcgttccct gtatcgagtt atctccttct ctaccgggaa actgggtcccc atcgccatcc 240
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 caaaatcgaa gcccggcgtt gtcgggctac agggttcgcc tcctccgcct gagaaggcaa 360
 cctcagcgcc cccccggcg gccagccga gcgcacacct caactcctgc tcgcattatt 420
 gacaaatatt accccctaata gagtttgtgt taagcgtttg gataaaagga ggaatgcaac 480
 aattatacag aaaacaagag 500

<210> 163
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 163

Pro Ala Lys Pro Ala Ile Ile Arg Ala Asn Arg Ser Arg Ser Ala Thr
 1 5 10 15

Gly Arg Ala Ser Pro Pro His Ser Ser Thr Ser Trp Arg Gly Ala Ser
 20 25 30

Pro Arg Leu Thr Thr Pro Thr Ser Leu Cys Val Arg Ser Trp His Cys
 35 40 45

Val Ser Gly
50

<210> 164
<211> 869
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (869)..(869)
<223> n = unknown

<400> 164
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tctccctccc gagaacagca gaaagggggg actcgacaga atgacctctg tttccccaag 180
gaagtgcact ctgacgataa ctcggggagg gacgagaagg gccgctcttt cggagagcgg 240
ccgccgcccc tggagtaggg gactcagtgg ccacgaaggc cttccctgct cgcgaccttt 300
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gcgaggggctc tgactctgcy gttcagggttt gaaagtcctt tggaagctcg caagtgggtg 420
tctcccacca cctgctcggg catagcagga agaaggcgca gtgagggcgg gagtctggat 480
gagcgggagag tagccaccgc ggagaagagt gcgggcttgc aggagccaac gaagataact 540
cgaaatgtgg gcaggcaggg gtcgggtgggt cttgcaaaag tgggaaagca cgagaaaaga 600
acaatgttcc gcgtccgctt agaatacgga aacaagttag ctttaaagga acaatactca 660
ttctcattac ccctgtccag gaagaaagag tgcttgatct tgcttgcttc ccagggtccgc 720
tgggcttgga gagccagaaa gagggctact tggatcccca gccaacgcca gtgggtctgtc 780
ccccagcga agcacttctg gccttgggtg gatccccatt ccttttctca aatacaaaat 840
cttatgagtc ctcggacagg aattacatn 869

<210> 165
<211> 85
<212> PRT
<213> Homo sapiens

<400> 165

Ser Gly Ala Cys Lys Ala Val Gly Arg Arg Ser Gly Arg Trp Pro Leu

Phe Ala Ser Leu Leu His Phe Leu Glu Pro Ala Glu Phe Ala Lys Arg

1 5 10 15

Ser Ile Lys Gly Lys Thr His
20

<210> 168

<211> 484

<212> DNA

<213> Homo sapiens

<400> 168

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gtttcacttc aacctcacac ccaggaaccc attcaaattc ctacatttcg gtatccttag 180
tcgaactaac ttcctgtgcc ggaagctttt gtctgtctca gtgacttctt tctttaacaa 240
attcccttca tctccccctt gagtcaaagc ccattggggtc cccaggaggc atgcaatatt 300
taccaagggc tcttccccgt tttcctgcct ctgtctggca gttgtttgcc tttactttta 360
ggttttagt cacagcctgt tttttcttcc ttggacacac cagcttttct gaatggtagg 420
attatttaca gtagaattaa ccttgtcctt caccocgaga actgagcttg aaattcacta 480
atca 484

<210> 169

<211> 48

<212> PRT

<213> Homo sapiens

<400> 169

Met Gly Ser Pro Gly Gly Met Gln Tyr Leu Pro Arg Ala Leu Pro Arg
1 5 10 15

Phe Pro Ala Ser Val Trp Gln Leu Phe Ala Phe Thr Phe Arg Phe Val
20 25 30

Val Thr Ala Cys Phe Phe Phe Leu Gly His Thr Ser Phe Ser Glu Trp
35 40 45

<210> 170

<211> 3941

<212> DNA

<213> Homo sapiens

<400> 170
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 acatccctaa gaactctcac cccattatct ttgagcacca gcacttcatt gactacaacc 180
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 tcatcttctc cctccatcca aagtacagaa acctcatccc ttgtgggcac cacctctccc 300
 accatgtcca ctgtgagagc gaccctcaga agtactgaga acacccaat cagttccttt 360
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 tctgccactg ggacccaaac atcccctgta cctactactg tcacctttgg aagtatggat 480
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 acatcacagt ttctattcc tagcacacat tcctccaccc ttcaaacaac tccttcaatc 600
 ccctctttgc aaacttcaact cacatctaca agtgagttca ctacagaatc tttcactagg 660
 ggaagtacgt ctacaaatgc aatcttgact tcttttagta ccatcatctg gtcctcaaca 720
 cccactatta tcatgtctc ttctccatct tctgccagca taactccagt gttcgtact 780
 accattcatt ctgttcttc gtcaccatac attttcagta cagaaaatgt gggctccgct 840
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 accacacagt ccagttgac caccactgca ggcacctgtg acaatggtgg cacctgggaa 1560
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tacagggatt tcaacaagac cttctggaat cagatgcaga agatttttgc agacatgcag	1860
ggcttcacct tcaaggggtgt ggagatcctg tccctgagga atggcagcat cgtggtggac	1920
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aagaccacgc tgaaggagg gctccagaac gccagccagg atgcgaacag ctgccaggac	2040
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ggtttcgagg acgacggaac agacaaggat acaaatttcc atgtggcctt ggagaacgtg	2580
gacaccacta tgaaggtgca catcaagaga cccgagatga cctcgtcctc agtgtgagcc	2640
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cccctcctcc cccctctctc cctggtgtca actcgattcc tgcgtaact ctgagccctg 3840
aaatcctcag tctccttggc ggggaagatt ggctttggg acaggaagtc ggcacatctc 3900
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<210> 171
<211> 878
<212> PRT
<213> Homo sapiens

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<400> 171

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```

Thr Ile Tyr Ser Thr Val Ser Ser Ser Thr Thr Ala Ile Thr Ser Pro
1           5           10           15

```

```

Phe Thr Thr Ala Glu Thr Gly Val Thr Ser Thr Pro Ser Ser Pro Ser
          20           25           30

```

```

Ser Leu Ser Thr Asp Ile Pro Thr Thr Ser Leu Arg Thr Leu Thr Pro
          35           40           45

```

```

Leu Ser Leu Ser Thr Ser Thr Ser Leu Thr Thr Thr Thr Asp Leu Pro
          50           55           60

```

```

Ser Ile Pro Thr Asp Ile Ser Ser Leu Pro Thr Pro, Ile His Ile Ile
65           70           75           80

```

```

Ser Ser Ser Pro Ser Ile Gln Ser Thr Glu Thr Ser Ser Leu Val Gly
          85           90           95

```

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Thr Thr Ser Pro Thr Met Ser Thr Val Arg Ala Thr Leu Arg Ser Thr
          100           105           110

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Glu Asn Thr Pro Ile Ser Ser Phe Ser Thr Ser Ile Val Val Thr Pro
 115 120 125
 Glu Thr Pro Thr Thr Gln Ala Pro Pro Val Leu Met Ser Ala Thr Gly
 130 135 140
 Thr Gln Thr Ser Pro Val Pro Thr Thr Val Thr Phe Gly Ser Met Asp
 145 150 155 160
 Ser Ser Thr Ser Thr Leu His Thr Leu Thr Pro Ser Thr Ala Leu Ser
 165 170 175
 Lys Ile Met Ser Thr Ser Gln Phe Pro Ile Pro Ser Thr His Ser Ser
 180 185 190
 Thr Leu Gln Thr Thr Pro Ser Ile Pro Ser Leu Gln Thr Ser Leu Thr
 195 200 205
 Ser Thr Ser Glu Phe Thr Thr Glu Ser Phe Thr Arg Gly Ser Thr Ser
 210 215 220
 Thr Asn Ala Ile Leu Thr Ser Phe Ser Thr Ile Ile Trp Ser Ser Thr
 225 230 235 240
 Pro Thr Ile Ile Met Ser Ser Ser Pro Ser Ser Ala Ser Ile Thr Pro
 245 250 255
 Val Phe Ala Thr Thr Ile His Ser Val Pro Ser Ser Pro Tyr Ile Phe
 260 265 270
 Ser Thr Glu Asn Val Gly Ser Ala Ser Ile Thr Ala Phe Pro Ser Leu
 275 280 285
 Ser Ser Ser Ser Thr Thr Ser Thr Ser Pro Thr Ser Ser Ser Leu Thr
 290 295 300
 Thr Ala Leu Thr Glu Ile Thr Pro Phe Ser Tyr Ile Ser Leu Pro Ser
 305 310 315 320
 Thr Thr Pro Cys Pro Gly Thr Ile Thr Ile Thr Ile Val Pro Ala Ser
 325 330 335

Pro Thr Asp Pro Cys Val Glu Met Asp Pro Ser Thr Glu Ala Thr Ser
340 345 350

Pro Pro Thr Thr Pro Leu Thr Val Phe Pro Phe Thr Thr Glu Met Val
355 360 365

Thr Cys Pro Ser Ser Ile Ser Met Gln Thr Thr Leu Ala Thr His Met
370 375 380

Asp Thr Ser Ser Met Thr Pro Glu Ser Glu Ser Ser Ile Ile Pro Asn
385 390 395 400

Ala Ser Ser Ser Thr Gly Thr Gly Thr Val Pro Thr Asn Thr Val Phe
405 410 415

Thr Ser Thr Arg Leu Pro Thr Ser Glu Thr Trp Leu Ser Asn Asn Ser
420 425 430

Val Ile Pro Thr Pro Leu Pro Gly Val Ser Thr Ile Pro Leu Thr Met
435 440 445

Lys Pro Ser Ser Ser Leu Pro Thr Ile Leu Arg Thr Ser Ser Lys Ser
450 455 460

Thr His Pro Ser Pro Pro Thr Ala Arg Thr Ser Glu Thr Ser Val Ala
465 470 475 480

Thr Thr Gln Thr Pro Thr Thr Leu Thr Thr Arg Arg Thr Thr Pro Ile
485 490 495

Thr Ser Trp Met Thr Thr Gln Ser Thr Leu Thr Thr Thr Ala Gly Thr
500 505 510

Cys Asp Asn Gly Gly Thr Trp Glu Gln Gly Gln Cys Ala Cys Leu Pro
515 520 525

Gly Phe Ser Gly Asp Arg Cys Gln Leu Gln Thr Arg Cys Gln Asn Gly
530 535 540

Gly Gln Trp Asp Gly Leu Lys Cys Gln Cys Pro Ser Thr Phe Tyr Gly
545 550 555 560

Ser Ser Cys Glu Phe Ala Val Glu Gln Val Asp Leu Asp Val Val Glu
 565 570 575
 Thr Glu Val Gly Met Glu Val Ser Val Asp Gln Gln Phe Ser Pro Asp
 580 585 590
 Leu Asn Asp Asn Thr Ser Gln Ala Tyr Arg Asp Phe Asn Lys Thr Phe
 595 600 605
 Trp Asn Gln Met Gln Lys Ile Phe Ala Asp Met Gln Gly Phe Thr Phe
 610 615 620
 Lys Gly Val Glu Ile Leu Ser Leu Arg Asn Gly Ser Ile Val Val Asp
 625 630 635 640
 Tyr Leu Val Leu Leu Glu Met Pro Phe Ser Pro Gln Leu Glu Ser Glu
 645 650 655
 Tyr Glu Gln Val Lys Thr Thr Leu Lys Glu Gly Leu Gln Asn Ala Ser
 660 665 670
 Gln Asp Ala Asn Ser Cys Gln Asp Ser Gln Thr Leu Cys Phe Lys Pro
 675 680 685
 Asp Ser Ile Lys Val Asn Asn Asn Ser Lys Thr Glu Leu Thr Pro Glu
 690 695 700
 Ala Ile Cys Arg Arg Ala Ala Pro Thr Gly Tyr Glu Glu Phe Tyr Phe
 705 710 715 720
 Pro Leu Val Glu Ala Thr Arg Leu Arg Cys Val Thr Lys Cys Thr Ser
 725 730 735
 Gly Val Asp Asn Ala Ile Asp Cys His Gln Gly Gln Cys Val Leu Glu
 740 745 750
 Thr Ser Gly Pro Ala Cys Arg Cys Tyr Ser Thr Asp Thr His Trp Phe
 755 760 765
 Ser Gly Pro Arg Cys Glu Val Ala Val His Trp Arg Ala Leu Val Gly
 770 775 780

Gly Leu Thr Ala Gly Ala Ala Leu Leu Val Leu Leu Leu Leu Ala Leu
785 790 795 800

Gly Val Arg Ala Val Arg Ser Gly Trp Trp Gly Gly Gln Arg Arg Gly
805 810 815

Arg Ser Trp Asp Gln Asp Arg Lys Trp Phe Glu Thr Trp Asp Glu Glu
820 825 830

Val Val Gly Thr Phe Ser Asn Trp Gly Phe Glu Asp Asp Gly Thr Asp
835 840 845

Lys Asp Thr Asn Phe His Val Ala Leu Glu Asn Val Asp Thr Thr Met
850 855 860

Lys Val His Ile Lys Arg Pro Glu Met Thr Ser Ser Ser Val
865 870 875

<210> 172
<211> 538
<212> DNA
<213> Homo sapiens

<400> 172
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 atttttgaaa gccagaaaat ctaattatgc tatagcccaa ctacctaatag ctttctttat 180
 ccataagtaa ctttgcttca atttcttgat gttgggtttc atctcactga ctttgggctt 240
 ctaagacaca tgggaatact tatatcatct tggcttcttt ggggtcaaatac aaacagtaga 300
 gctaaagtta ttcaaataca ttcagattac acagatccct tatgaattac tagtatcata 360
 gtaggaagaa aaagatacaa gaaaaataca tcctagaact cattatcaaa attattggtg 420
 tatagtctat actagcatag agtagctttc tcaacctgct atataaaatt actagcaaga 480
 aaaaaagggtg caagaataag atttatggct gaagtggctt ggtgtcttga ttccctat 538

<210> 173
<211> 31
<212> PRT
<213> Homo sapiens

<400> 173

Met Gly Ile Leu Ile Ser Ser Trp Leu Leu Trp Val Lys Ser Asn Ser
 1 5 10 15

Arg Ala Lys Val Ile Gln Ile His Ser Asp Tyr Thr Asp Pro Leu
 20 25 30

<210> 174
 <211> 2609
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc feature
 <222> (2025)..(2025)
 <223> n = unknown

<220>
 <221> misc feature
 <222> (2036)..(2036)
 <223> n = unknown

<220>
 <221> misc feature
 <222> (2164)..(2164)
 <223> n = unknown

<220>
 <221> misc feature
 <222> (2264)..(2264)
 <223> n = unknown

<400> 174
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 ctcttgggggt aggtgtgtgt ttttcacatc ttaaaggctc acagaccctg cgctggacaa 120
 atgttccatt cctgaaggac ctctccagaa tccggattgc tgaatcttcc ctgttgcccta 180
 gaagggctcc aaaccacctc ttgacaatgg gaaactgggt ggtaaccac tggttttcag 240
 ttttgtttct ggttgtttgg ttagggctga atgttttcct gtttgtggat gccttcctga 300
 aatatgagaa ggccgacaaa tactactaca caagaaaaat ccttgggtca acattggcct 360
 gtgcccagagc gtctgctctc tgcttgaatt ttaacagcac gctgatcctg cttcctgtgt 420
 gtgcgaatct gctgtccttc ctgaggggca cctgctcatt ttgcagccgc aactgagaa 480
 agcaattgga tcacaacctc acctccaca agctggtggc ctatatgatc tgcctacata 540

cagctattca catcattgca cacctgttta actttgactg ctatagcaga agccgacagg	600
ccacagatgg ctcccttgcc tccattctct ccagcctatc tcatgatgag aaaaaggggg	660
gttcttggtt aaatcccatc cagtcccgaa acacgacagt ggagtatgtg acattcacca	720
gcgttgctgg tctcactgga gtgatcatga caatagcctt gattctcatg gtaacttcag	780
ctactgagtt catccggagg agttattttg aagtcttctg gtatactcac caccttttta	840
tcttctatat ccttggctta gggattcacg gcattggttg aattgtccgg ggtcaaacag	900
aggagagcat gaatgagagt catcctcgca agtgtgcaga gtcttttgag atgtgggatg	960
atcgtgactc ccactgtagg cgcctaagt ttgaaggga tccccctgag tcttgggaagt	1020
ggatccttgc accggtcatt ctttatactt gtgaaaggat cctccggttt taccgctccc	1080
agcagaaggt tgtgattacc aaggttgtta tgcacccatc caaagttttg gaattgcaga	1140
tgaacaagcg tggcttcagc atggaagtgg ggcagtatat ctttgttaat tgcccccaa	1200
tctctctcct ggaatggcat ctttttactt tgacctctgc tccagaggaa gatttcttct	1260
ccattcatat ccgagcagca ggggactgga cagaaaatct cataagggtt ttogaacaac	1320
aatattcacc aattcccagg attgaagtgg atggtccctt tggcacagcc agtgaggatg	1380
ttttccagta tgaagtggct gtgctggttg gagcaggaat tggggtcacc ccttttgctt	1440
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agatctatth ctactggatc tgcagggaga cagggtgcctt ttcttggttc aacaacctgt	1560
tgacttccct ggaacaggag atggaggaat taggcaaagt gggttttcta aactaccgtc	1620
tcttcctcac cggatgggac agcaatattg ttggtcatgc agcattaaac tttgacaagg	1680
ccactgacat cgtgacaggc ctgaaacaga aaacctcctt tgggagacca atgtgggaca	1740
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gccctcggac tttggcaaag agcctgcgca aatgctgtca ccgatattcc agtctggatc	1860
ctagaaaggc tcaattctac ttcaacaaag aaaatttttg agttatagga ataaggacgg	1920
taatctgcat tttgtctctt tgtatcttca gtaattgagt tataggaata aggacggtaa	1980
tctgcatttt gtctctttgt atcttcagta atttacttgg tctcttcagg tttgancagt	2040
cacttttagga taagaatgtg cctctcaagc cttgactccc tggatattctt tttttgattg	2100
cattcaactt cgttacttga gcttcagcaa cttagaact tctgaagtcc ttaaagttct	2160
gaantttcta aagcccatgg atcctttctc agaaaaataa ctgtaaatct ttctggacag	2220

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ccatgactgt agcaaggctt gatagcagaa gtttggtggt tcanaattat acaactaatc 2280
ccaggtgatt ttatcaattc cagtgttacc atctcctgag ttttggtttg taatcttttg 2340
tccctccac cccacagaa gattttaagt agggtgactt tttaaataaa aatttattga 2400
ataattaatg ataaaacata ataataaaca taaataataa acaaaattac cgagaacccc 2460
atccccatat aacaccaaca gtgtacatgt ttactgtcac ttttgatatg gtttatccag 2520
tgtgaacagc aatttattat ttttgctcat caaaaaataa aggatttttt ttcacttgaa 2580
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2609

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<210> 175
<211> 658
<212> DNA
<213> Homo sapiens

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<400> 175
ggacctctcc agaatccgga ttgctgaatc ttccctgttg cctagaaggg ctccaaacca 60
cctcttgaca atgggaaact gggtggttaa ccactggttt tcagttttgt ttctggttgt 120
ttggttaggg ctgaatgttt tcctgtttgt ggatgccttc ctgaaatatg agaaggccga 180
caaatactac tacacaagaa aaatccttgg gtcaacattg gcctgtgcc gagcgtctgc 240
tctctgcttg aattttaaca gcacgctgat cctgcttcct gtgtgtcgca atctgctgtc 300
cttcctgagg ggcacctgct catTTTgcag ccgcacactg agaaagcaat tggatcacia 360
cctcaccttc cacaagctgg tggcctatat gatctgccta catacagcta ttcacatcat 420
tgcacacctg ttttaactttg actgctatag cagaagccga caggccacag atggctccct 480
tgcctccatt ctctccagcc tatctcatga tgagaaaaag gggggttctt ggctaaatcc 540
catccatccc catataacac caacagtgt catgtttact gtcacttttg atatggtctt 600
atccagtgtg aacagcaatt tattatTTTT gctcatcaaa aaataaagga ttttcttc 658

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<210> 176
<211> 564
<212> PRT
<213> Homo sapiens

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<400> 176

```

```

Met Gly Asn Trp Val Val Asn His Trp Phe Ser Val Leu Phe Leu Val
1           5           10           15

```

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Val Trp Leu Gly Leu Asn Val Phe Leu Phe Val Asp Ala Phe Leu Lys

```

	20		25		30												
Tyr	Glu	Lys	Ala	Asp	Lys	Tyr	Tyr	Tyr	Thr	Arg	Lys	Ile	Leu	Gly	Ser		
		35					40					45					
Thr	Leu	Ala	Cys	Ala	Arg	Ala	Ser	Ala	Leu	Cys	Leu	Asn	Phe	Asn	Ser		
	50					55					60						
Thr	Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Leu	Leu	Ser	Phe	Leu	Arg		
65					70				75						80		
Gly	Thr	Cys	Ser	Phe	Cys	Ser	Arg	Thr	Leu	Arg	Lys	Gln	Leu	Asp	His		
				85					90					95			
Asn	Leu	Thr	Phe	His	Lys	Leu	Val	Ala	Tyr	Met	Ile	Cys	Leu	His	Thr		
			100					105					110				
Ala	Ile	His	Ile	Ile	Ala	His	Leu	Phe	Asn	Phe	Asp	Cys	Tyr	Ser	Arg		
		115					120					125					
Ser	Arg	Gln	Ala	Thr	Asp	Gly	Ser	Leu	Ala	Ser	Ile	Leu	Ser	Ser	Leu		
	130					135					140						
Ser	His	Asp	Glu	Lys	Lys	Gly	Gly	Ser	Trp	Leu	Asn	Pro	Ile	Gln	Ser		
145					150					155					160		
Arg	Asn	Thr	Thr	Val	Glu	Tyr	Val	Thr	Phe	Thr	Ser	Val	Ala	Gly	Leu		
				165					170					175			
Thr	Gly	Val	Ile	Met	Thr	Ile	Ala	Leu	Ile	Leu	Met	Val	Thr	Ser	Ala		
		180						185					190				
Thr	Glu	Phe	Ile	Arg	Arg	Ser	Tyr	Phe	Glu	Val	Phe	Trp	Tyr	Thr	His		
		195					200					205					
His	Leu	Phe	Ile	Phe	Tyr	Ile	Leu	Gly	Leu	Gly	Ile	His	Gly	Ile	Gly		
	210					215					220						
Gly	Ile	Val	Arg	Gly	Gln	Thr	Glu	Glu	Ser	Met	Asn	Glu	Ser	His	Pro		
225					230					235					240		
Arg	Lys	Cys	Ala	Glu	Ser	Phe	Glu	Met	Trp	Asp	Asp	Arg	Asp	Ser	His		

232

465 470 475 480
 Ile Val Gly His Ala Ala Leu Asn Phe Asp Lys Ala Thr Asp Ile Val
 485 490 495
 Thr Gly Leu Lys Gln Lys Thr Ser Phe Gly Arg Pro Met Trp Asp Asn
 500 505 510
 Glu Phe Ser Thr Ile Ala Thr Ser His Pro Lys Ser Val Val Gly Val
 515 520 525
 Phe Leu Cys Gly Pro Arg Thr Leu Ala Lys Ser Leu Arg Lys Cys Cys
 530 535 540
 His Arg Tyr Ser Ser Leu Asp Pro Arg Lys Val Gln Phe Tyr Phe Asn
 545 550 555 560
 Lys Glu Asn Phe

<210> 177
 <211> 191
 <212> PRT
 <213> Homo sapiens

<400> 177

Met Gly Asn Trp Val Val Asn His Trp Phe Ser Val Leu Phe Leu Val
 1 5 10 15
 Val Trp Leu Gly Leu Asn Val Phe Leu Phe Val Asp Ala Phe Leu Lys
 20 25 30
 Tyr Glu Lys Ala Asp Lys Tyr Tyr Tyr Thr Arg Lys Ile Leu Gly Ser
 35 40 45
 Thr Leu Ala Cys Ala Arg Ala Ser Ala Leu Cys Leu Asn Phe Asn Ser
 50 55 60
 Thr Leu Ile Leu Leu Pro Val Cys Arg Asn Leu Leu Ser Phe Leu Arg
 65 70 75 80
 Gly Thr Cys Ser Phe Cys Ser Arg Thr Leu Arg Lys Gln Leu Asp His
 85 90 95

Asn Leu Thr Phe His Lys Leu Val Ala Tyr Met Ile Cys Leu His Thr
100 105 110

Ala Ile His Ile Ile Ala His Leu Phe Asn Phe Asp Cys Tyr Ser Arg
115 120 125

Ser Arg Gln Ala Thr Asp Gly Ser Leu Ala Ser Ile Leu Ser Ser Leu
130 135 140

Ser His Asp Glu Lys Lys Gly Gly Ser Trp Leu Asn Pro Ile His Pro
145 150 155 160

His Ile Thr Pro Thr Val Tyr Met Phe Thr Val Thr Phe Asp Met Val
165 170 175

Leu Ser Ser Val Asn Ser Asn Leu Leu Phe Leu Leu Ile Lys Lys
180 185 190

<210> 178
<211> 1683
<212> DNA
<213> Homo sapiens

<400> 178
aagcctcttt catcggggca cagacttctt ttacttctt ctttttgccc tctcgctcc 60
tcctcctggg aagaagcgga ggcgcggcg gtcggccggg atagcaacag gccgggccac 120
tgaggcgggt cggaaggtt ctgtctggga gtgcggaact ggggccgggt tgggtgtactg 180
ctcggagcaa tggagccagc cttcggggag gtgaaccagc tgggaggagt gttcgtgaac 240
gggaggccgc tgccaacgc catcgggctt cgcctcgtg aactggccca actgggcac 300
cgaccgtgtg acatcagccg ccagctacgg gtctcgcacg gctgcgtcag caagatcctg 360
gcgcgataca acgagacggg ctcgatcttg ccaggagcca tcgggggcag caagccccgg 420
gtcactaccc ccaccgtggt gaaacacatc cggacctaca agcagagaga ccccggcac 480
ttcgctggg agatccggga ccgcctgctg gcggacggcg tgtgcgacaa gtacaatgtg 540
ccctccgtga gctccatcag ccgcattctg cgcaacaaga tcggcaactt ggcccagcag 600
ggtcattacg actcatacaa gcagcaccag ccgacgccgc agccagcgt gccctacaac 660
cacatctact cgtaccccag ccctatcacg gcggcgccg ccaagggtgcc cagccaccc 720
ggggtgcctg ccatccccgg ttcggtggcc atgccgcgca cctggccctc ctgcactcc 780


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gtcaccgaca tcctgggcat ccgctccatc accgaccaag tgagcgacag ctccccctac      840
cacagcccca aggtggagga gtggagcagc ctggggccgca acaacttccc cgccgccgcc      900
ccgcatgcgg tgaacgggtt ggagaaggga gccctggagc aggaagccaa gtacggtcag      960
gcaccaaagt gtctcccagc tgtgggcagt tttgtgtcag catccagcat ggctccttac     1020
cctaccccag cccaagtgtc gccttacatg acctacagtg ctgctccttc tggttatggt     1080
gctggacatg ggtggcaaca tgctgggggc acctcattgt ctccccacaa ctgtgacatt     1140
ccggcatcgc tggcgttcaa gggaatgcag gcagccagag aaggtagtca ttctgtcacg     1200
gcttccgcgc tctgatggga aattccgtct ccagcagctt caccggggtc tccctgtctc     1260
agcacctcct cccccaattc ccaggctctca catcccaccc ctctgccct ccaacccttc     1320
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aacaataagc attgaatgag acatttgtgt tgccacata ctgtcttaac ataacaaaga     1500
aacctacacc cctcaaaggg tttaaggaac ttacaaaact agtctttggt aaaaccacat     1560
gtgtatatatt attctaaatc aacctgaact ttgaaatgt gcaattgttg agattttgca     1620
aatcaataa aggaaaatac ttatagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa     1680
aaa                                                                1683

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<210> 179
 <211> 341
 <212> PRT
 <213> Homo sapiens

<400> 179

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Met Glu Pro Ala Phe Gly Glu Val Asn Gln Leu Gly Gly Val Phe Val
1           5           10           15

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Asn Gly Arg Pro Leu Pro Asn Ala Ile Arg Leu Arg Ile Val Glu Leu
20           25           30

```

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Ala Gln Leu Gly Ile Arg Pro Cys Asp Ile Ser Arg Gln Leu Arg Val
35           40           45

```

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Ser His Gly Cys Val Ser Lys Ile Leu Ala Arg Tyr Asn Glu Thr Gly
50           55           60

```

Ser Ile Leu Pro Gly Ala Ile Gly Gly Ser Lys Pro Arg Val Thr Thr
65 70 75 80

Pro Thr Val Val Lys His Ile Arg Thr Tyr Lys Gln Arg Asp Pro Gly
85 90 95

Ile Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu Ala Asp Gly Val Cys
100 105 110

Asp Lys Tyr Asn Val Pro Ser Val Ser Ser Ile Ser Arg Ile Leu Arg
115 120 125

Asn Lys Ile Gly Asn Leu Ala Gln Gln Gly His Tyr Asp Ser Tyr Lys
130 135 140

Gln His Gln Pro Thr Pro Gln Pro Ala Leu Pro Tyr Asn His Ile Tyr
145 150 155 160

Ser Tyr Pro Ser Pro Ile Thr Ala Ala Ala Lys Val Pro Thr Pro
165 170 175

Pro Gly Val Pro Ala Ile Pro Gly Ser Val Ala Met Pro Arg Thr Trp
180 185 190

Pro Ser Ser His Ser Val Thr Asp Ile Leu Gly Ile Arg Ser Ile Thr
195 200 205

Asp Gln Val Ser Asp Ser Ser Pro Tyr His Ser Pro Lys Val Glu Glu
210 215 220

Trp Ser Ser Leu Gly Arg Asn Asn Phe Pro Ala Ala Ala Pro His Ala
225 230 235 240

Val Asn Gly Leu Glu Lys Gly Ala Leu Glu Gln Glu Ala Lys Tyr Gly
245 250 255

Gln Ala Pro Asn Gly Leu Pro Ala Val Gly Ser Phe Val Ser Ala Ser
260 265 270

Ser Met Ala Pro Tyr Pro Thr Pro Ala Gln Val Ser Pro Tyr Met Thr
275 280 285

Tyr Ser Ala Ala Pro Ser Gly Tyr Val Ala Gly His Gly Trp Gln His
 290 295 300

Ala Gly Gly Thr Ser Leu Ser Pro His Asn Cys Asp Ile Pro Ala Ser
 305 310 315 320

Leu Ala Phe Lys Gly Met Gln Ala Ala Arg Glu Gly Ser His Ser Val
 325 330 335

Thr Ala Ser Ala Leu
 340

<210> 180

<211> 1253

<212> DNA

<213> Homo sapiens

<400> 180

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tgcccgcaga cctagtgggc gagaggagtg cacaaagcaa agcagcggag tccttgaggg      180
agctgcgggc ctgcatcagc accctggtgg atcggcaccg ggaggcccag cagggtgctgg      240
ctcggctgca agaagaaaac cagcagttgc gggggctcctt gtccccgtgt agggagccag      300
gcacctcctt aaaggcccca gcatcccccc aagtggccgc tctggagcaa gacctgggga      360
agctggagga agagctgcgg gcagttcagg ccacgatgag cgggaagagc caggagatcg      420
gaaagctgaa gcagctgctc taccaagcca cagaggaagt ggctgagcta agggcccggg      480
aggcagccag cctacggcaa cagcagaaaa ctcgggggttc gctggtggcc caggctcagg      540
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cagccgaaca agagcgccag gccagcgaga tgcgggggcg ctccgagcag tttgagaaaa      720
cggcagagct gctgaaagag aagatggagc atctcattgg ggcttgccga gacaagggaag      780
ccaagatcaa ggagttgttg aagaagctgg agcagctttc agaagaggtt ctagcaattc      840
ggggagaaaa tgctgcctt gccctgcagc tgcaggattc ccagaagaac catgaagaga      900
tcatctccac ctacaggaat catctactga atgctgctcg gggttacatg gaacatgaag      960
tgtacaatat cctgctgcaa atccttagca tggaagagga gtgaggcagc ctcaactgtgt     1020

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gccctcaggg atacgagatt ctctgttgga ataagaaacc ctggttgaca gaggttcat 1080
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 acattatgga cctcagacct gagaacctgg accctggaat cagcatggat gagaccagag 1200
 gaggtatgga tggaacaag ctctatggaa aataaagcat gaggcaggac ggg. 1253

<210> 181
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 181

Met Glu Lys Glu Ala Thr Glu Lys Leu Arg Lys Leu Leu Ala Ser Gln
 1 5 10 15

Ser Ser Gly Leu Arg Gly Leu Trp Asp Cys Leu Pro Ala Asp Leu Val
 20 25 30

Gly Glu Arg Ser Ala Gln Ser Lys Ala Ala Glu Ser Leu Glu Glu Leu
 35 40 45

Arg Ala Cys Ile Ser Thr Leu Val Asp Arg His Arg Glu Ala Gln Gln
 50 55 60

Val Leu Ala Arg Leu Gln Glu Glu Asn Gln Gln Leu Arg Gly Ser Leu
 65 70 75 80

Ser Pro Cys Arg Glu Pro Gly Thr Ser Leu Lys Ala Pro Ala Ser Pro
 85 90 95

Gln Val Ala Ala Leu Glu Gln Asp Leu Gly Lys Leu Glu Glu Glu Leu
 100 105 110

Arg Ala Val Gln Ala Thr Met Ser Gly Lys Ser Gln Glu Ile Gly Lys
 115 120 125

Leu Lys Gln Leu Leu Tyr Gln Ala Thr Glu Glu Val Ala Glu Leu Arg
 130 135 140

Ala Arg Glu Ala Ala Ser Leu Arg Gln His Glu Lys Thr Arg Gly Ser
 145 150 155 160

Leu Val Ala Gln Ala Gln Ala Trp Gly Gln Glu Leu Lys Ala Leu Leu
 165 170 175

Glu Lys Tyr Asn Thr Ala Cys Arg Glu Val Gly Arg Leu Arg Glu Ala
 180 185 190

Val Ala Glu Glu Arg Arg Arg Ser Gly Asp Leu Ala Ala Gln Ala Ala
 195 200 205

Glu Gln Glu Arg Gln Ala Ser Glu Met Arg Gly Arg Ser Glu Gln Phe
 210 215 220

Glu Lys Thr Ala Glu Leu Leu Lys Glu Lys Met Glu His Leu Ile Gly
 225 230 235 240

Ala Cys Arg Asp Lys Glu Ala Lys Ile Lys Glu Leu Leu Lys Lys Leu
 245 250 255

Glu Gln Leu Ser Glu Glu Val Leu Ala Ile Arg Gly Glu Asn Ala Arg
 260 265 270

Leu Ala Leu Gln Leu Gln Asp Ser Gln Lys Asn His Glu Glu Ile Ile
 275 280 285

Ser Thr Tyr Arg Asn His Leu Leu Asn Ala Ala Arg Gly Tyr Met Glu
 290 295 300

His Glu Val Tyr Asn Ile Leu Leu Gln Ile Leu Ser Met Glu Glu Glu
 305 310 315 320

<210> 182

<211> 2839

<212> DNA

<213> Homo sapiens

<400> 182

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<210> 183

<211> 338

<212> PRT

<213> Homo sapiens

<400> 183

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Met Leu Gln Lys Pro Lys Ser Val Lys Leu Arg Ala Leu Arg Ser Pro
1           5           10           15

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Arg Lys Phe Gly Val Ala Gly Arg Ser Cys Gln Glu Val Leu Arg Lys
          20           25           30

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Gly Cys Leu Arg Phe Gln Leu Pro Glu Arg Gly Ser Arg Leu Cys Leu
          35           40           45

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Tyr Glu Asp Gly Thr Glu Leu Thr Glu Asp Tyr Phe Pro Ser Val Pro
50           55           60

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Asp Asn Ala Glu Leu Val Leu Leu Thr Leu Gly Gln Ala Trp Gln Gly
65           70           75           80

```

Tyr Val Ser Asp Ile Arg Arg Phe Leu Ser Ala Phe His Glu Pro Gln
 85 90 95
 Val Gly Leu Ile Gln Ala Ala Gln Gln Leu Leu Cys Asp Glu Gln Ala
 100 105 110
 Pro Gln Arg Gln Arg Leu Leu Ala Asp Leu Leu His Asn Val Ser Gln
 115 120 125
 Asn Ile Ala Ala Glu Thr Arg Ala Glu Asp Pro Pro Trp Phe Glu Gly
 130 135 140
 Leu Glu Ser Arg Phe Gln Ser Lys Ser Gly Tyr Leu Arg Tyr Ser Cys
 145 150 155 160
 Glu Ser Arg Ile Arg Ser Tyr Leu Arg Glu Val Ser Ser Tyr Pro Ser
 165 170 175
 Thr Val Gly Ala Glu Ala Gln Glu Glu Phe Leu Arg Val Leu Gly Ser
 180 185 190
 Met Cys Gln Arg Leu Arg Ser Met Gln Tyr Asn Gly Ser Tyr Phe Asp
 195 200 205
 Arg Gly Ala Lys Gly Gly Ser Arg Leu Cys Thr Pro Glu Gly Trp Phe
 210 215 220
 Ser Cys Gln Gly Pro Phe Asp Met Asp Ser Cys Leu Ser Arg His Ser
 225 230 235 240
 Ile Asn Pro Tyr Ser Asn Arg Glu Ser Arg Ile Leu Phe Ser Thr Trp
 245 250 255
 Asn Leu Asp His Ile Ile Glu Lys Lys Arg Thr Ile Ile Pro Thr Leu
 260 265 270
 Val Glu Ala Ile Lys Glu Gln Asp Gly Arg Glu Val Asp Trp Glu Tyr
 275 280 285
 Phe Tyr Gly Leu Leu Phe Thr Ser Glu Asn Leu Lys Leu Val His Ile
 290 295 300

Val Cys His Lys Lys Thr Thr His Lys Leu Asn Cys Asp Pro Ser Arg
 305 310 315 320

Ile Tyr Lys Pro Gln Thr Arg Leu Lys Arg Lys Gln Pro Val Arg Lys
 325 330 335

Arg Gln

<210> 184
 <211> 435
 <212> DNA
 <213> Homo sapiens

<400> 184
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 tccactttat tctgtaacct tttcaactac cattttgaaa tttgctttta tccatgtggt 180
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 ctagtatgtc ctgtatctca agaggatctc atcagtggaa tcattagatc aaaggatatg 300
 actgttgctc agctctctgt gtgtatgtaa attaataggc tgtttatttg agcagttgta 360
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 ctgtcgtctt ctgcg 435

<210> 185
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 185

Met Ile Ala Arg His Arg Tyr Asp Phe Phe Leu Phe Phe Ser Phe Phe
 1 5 10 15

Phe Phe Leu His Ser Cys Tyr Leu Lys Val Ile Ser Asn Phe Phe Ser
 20 25 30

Ile Tyr Ile Phe Pro Gln Ala Leu Ser Thr Leu Phe Cys Asn Leu Phe
 35 40 45

Asn Tyr His Phe Glu Ile Cys Phe Tyr Pro Cys Gly Cys Leu
 50 55 60

<210> 186
 <211> 368
 <212> DNA
 <213> Homo sapiens

<400> 186
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 tctatggaaa ttgcctggaa gagtcagctg taagggatga gaatcctgag ggtaaaagag 180
 aaaagggaaa gactcctctt tgatcttatg aagctgaaat aacaagatct taaacatgag 240
 tgagaatctg ttgccccaac ctaagggtgac tttaaatcca aggtaaaaaa cacggcatgg 300
 gtattagttt gaataggga aatgagaact ctctttgagc tcaaaaaaaaa aaaaaaaaaa 360
 aaaaaaatg 368

<210> 187
 <211> 24
 <212> PRT
 <213> Homo sapiens

<400> 187

Phe Phe Phe Phe Phe Leu Gly Val Thr Ala Ala Phe Ile Asn Ile Arg
 1 5 10 15

Arg Ala Thr Val Gln Glu Val Gly
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<210> 188
 <211> 27
 <212> PRT
 <213> Homo sapiens

<400> 188

Met Trp Gly Gln Gln Arg Asp Cys Gly Arg Gly Arg Thr Ala Asp Leu
 1 5 10 15

Trp Lys Leu Pro Gly Arg Val Ser Cys Lys Gly
 20 25

<210> 189
 <211> 342
 <212> DNA
 <213> Homo sapiens

<400> 189
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 agatgacatg tgaataatga ccaaggagcc ggccctccaa gactacaggg aaaaataaca 120
 ggggcatccc aagaagaggg aagagctggc atgaggctct gctgcagagg cactgagggc 180
 aagtgaaga acagagagga gcaaagcgcg gctggagtga gaccagtgga ggcagcacgc 240
 agcacctcct gggtcactcc aagtgtgagg gcaggccctg gcacactgct tttcttaaga 300
 attaaaaaaaa aaaaaaaaaa aaaaaaaaaa aagtcgtatc ga 342

<210> 190
 <211> 19
 <212> PRT
 <213> Homo sapiens

<400> 190

Leu Leu Phe Leu Arg Ile Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
 1 5 10 15

Ser Tyr Arg

<210> 191
 <211> 159
 <212> DNA
 <213> Homo sapiens

<400> 191
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 agggaataga gaaaagatgt aaccagagga ggagaaagag attaaatgta tgtgaatgtt 120
 ttacaaaaaa aaaaaaaaaa aaaaaaaaag tcgtatcga 159

<210> 192
 <211> 18
 <212> PRT
 <213> Homo sapiens

<400> 192

Met Tyr Val Asn Val Leu Gln Lys Lys Lys Lys Lys Lys Lys Lys Ser
 1 5 10 15

Tyr Arg

<210> 193
 <211> 448
 <212> DNA
 <213> Homo sapiens

<400> 193
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 ttctagaagt ggaattgcca ggtcacgtgc attttacatt ttaatggata cccagtggca 180
 ggcatagtgt ttcctacata gcaggagctt cgtaaagatc tgtggcgtga ttacatgggtg 240
 ccagatggcc ctctagaaaa gggacaccat tcccactccc accaaggatg accagaagag 300
 ccaagaggtt tccatttctg tcaccaggtc acagcaacac taggtttcag gatggccact 360
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 gcaacgtccg ggccgagggt aacttctc 448

<210> 194
 <211> 29
 <212> PRT
 <213> Homo sapiens

<400> 194

Met Ile Leu Ile Glu Leu Phe Cys Met Ser Thr Ser Glu Gly Ser Phe
 1 5 10 15

Leu Glu Val Glu Leu Pro Gly His Val His Phe Thr Phe
 20 25

<210> 195
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 195
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 gcagctgcaa cttccatgaa tatttagcat atctgagcac agagaagact acggccagtc 180
 ctgatgcagc tggcagcccc ttctgtgggc aaaaacatct acacagcatg tgtatgtgtg 240
 tgagtatatg tgtctaattg ttttaagcca gtttcatgat caggtcatta atctgataag 300
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tgaccaggct taggaatagg aatacaaata ttggggcaga tagct

405

<210> 196
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 196

Met Glu Cys Pro Val Gly Val Trp Glu Leu Ser Gly Lys Arg Tyr Ser
 1 5 10 15

Ser Ser Cys Asn Phe His Glu Tyr Leu Ala Tyr Leu Ser Thr Glu Lys
 20 25 30

Thr Thr Ala Ser Pro Asp Ala Ala Gly Ser Pro Phe Cys Gly Gln Lys
 35 40 45

His Leu His Ser Met Cys Met Cys Val Ser Ile Cys Val
 50 55 60

<210> 197
 <211> 478
 <212> DNA
 <213> Homo sapiens

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<400> 197
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 acaggtagag agattgtgtg cctagtagtg tgcgagagga gataggaaaa taggctgaag 360
 aaagatgggtg gtagtttatt tccaattttt atggatacat aatagttgta catattttatg 420
 gggtagatat gatattttga tacaacata caacgtataa tgatcaaatac anggtaat 478

<210> 198

<211> 60
 <212> PRT
 <213> Homo sapiens
 <400> 198

Met Cys Ser Asp Gln Ile Arg Val Ile Ser Ile Ser Ile Ile Ser Asn
 1 5 10 15

Thr Tyr His Phe Phe Met Leu Glu Thr Phe Asn Asn Phe Leu Pro Ala
 20 25 30

Ile Ser Tyr Leu Lys Leu His Ile Ile Val Asn Tyr Ser His Pro Thr
 35 40 45

Val Val Gln Asp Ile Leu Asn Asn Lys Tyr Ile Ser
 50 55 60

<210> 199
 <211> 1372
 <212> DNA
 <213> Homo sapiens

<400> 199
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 aattctagac atcatacttt atacatttca aaataacttt tttactaatc acatctttca 420
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 gctcctcttc tttgttttct gtgaatggaa attagctcta gattagaggc ttgattaggt 780
 tcaacatttt tttttttttt ttttttggca agcagatatt tggttgtcct gttcttagta 840

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<210> 200
<211> 45
<212> PRT
<213> Homo sapiens

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<400> 200

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Met Pro Val Pro Ser Asp His Val Thr Gln Cys Val Ile Glu Ser Pro
1          5          10          15

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```

Leu Leu Phe Glu Lys Ile Ser Ser Gln Leu Phe Cys Leu Asn Trp Asp
          20          25          30

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Pro Asn Glu Val Leu Lys Met His Phe Val Leu Phe Asn
          35          40          45

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<210> 201
<211> 2518
<212> DNA
<213> Homo sapiens

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<400> 201

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<210> 202
 <211> 435
 <212> PRT
 <213> Homo sapiens

<400> 202

Met Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser Leu Gln Tyr Arg
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Val Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly Ser
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Glu Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu Glu
 35 40 45

Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile Val
 50 55 60

Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val Ser
 65 70 75 80

Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val Ala
 85 90 95

Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro Gly
 100 105 110

Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp
 115 120 125

Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser
 130 135 140
 Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu
 145 150 155 160
 Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly
 165 170 175
 Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe
 180 185 190
 Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile
 195 200 205
 Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser
 210 215 220
 Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly
 225 230 235 240
 Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Leu Cys Pro
 245 250 255
 Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser
 260 265 270
 Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser
 275 280 285
 Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser
 290 295 300
 Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp
 305 310 315 320
 Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His
 325 330 335
 Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser
 340 345 350

Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Val Ser
355 360 365

Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr
370 375 380

Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu
385 390 395 400

Tyr Glu Gly Ala Ala Ala Thr Asp Ile Val Asp Ser Gln Tyr Asp
405 410 415

Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro Val Ser Pro
420 425 430

Pro Ser Met
435

<210> 203
<211> 491
<212> DNA
<213> Homo sapiens

<400> 203
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tgcacgcccc cctcccccaa ggcttacagt ctgagggaaa aaaaccacag tccccacca 120
acctgggaca aaactagacg acctcatggg ggggatgagg ggaggagaaa cccccctcc 180
caaccagga agccagagaa cgccaccggg gcacacaggt cgcctctgct gagtctgtag 240
gttcgggtctg ggctgagcgc cagcagcaat ctggcctccc atcccttctt ctgggttctt 300
ttctcgagga gtaagcgtgc tcccaaagaa gtcgctagta tctgaggcca tctggtggag 360
agcagtggca tggttaaccga gggctcaaag tcgggctcgc attccgggga ctgcagaga 420
ctggactgcg cctgcggcaa ggaaggacgg agcagagccc cctgaggcgg agcgggagcc 480
agaccaagg a 491

<210> 204
<211> 79
<212> PRT
<213> Homo sapiens

<400> 204

Lys Ile Gln Gln Ser Phe Tyr Leu Ala Leu Trp Cys Arg Arg Ser Ala
1 5 10 15

Tyr Val Pro Ile Cys Thr Pro Pro Ser Pro Lys Ala Tyr Ser Leu Arg
20 25 30

Glu Lys Asn His Ser Pro His Pro Thr Trp Asp Lys Thr Arg Arg Pro
35 40 45

His Gly Gly Asp Ala Gly Arg Arg Asn Pro Pro Ser Gln Pro Arg Lys
50 55 60

Pro Glu Asn Ala Thr Gly Ala His Arg Ser Pro Leu Leu Ser Leu
65 70 75

<210> 205
<211> 500
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (482)..(482)
<223> n = unknown

<400> 205
gatgaaggcc agtaacatta cttgccattc attataactc acaattgctg aacaactaca 60
tggtctagac actgtgccaa attttctaca tttaaaagaa atttagttct atccataacc 120
attgcttggc gtttaaatta aaaaaaaaaa agttctaaca attccattct gtaggtgagt 180
gttagtattg tcattttata aatgagaaaa ctgaggctga ggcattaact tgcctaaaag 240
acacataacg tagcaagatt tgaactctga atctgtagtt ttcattatgg agcataacta 300
cgctgagacg acaaactctga aatctgccat aaaaaagatg actggtggaa tttatatttc 360
taatataaga acagaataga caacaaacag ctagacaaca aagaatctta cctgaacaca 420
gaagatggac ttgtggtaaa gtatatgaaa atgcctccaa gttccctgcc tccctatctt 480
tntaaaataa tattttcccc 500

<210> 206
<211> 30
<212> PRT
<213> Homo sapiens

<400> 206

Met Glu His Asn Tyr Ala Glu Thr Thr Asn Leu Lys Ser Ala Ile Lys
 1 5 10 15

Lys Met Thr Gly Gly Ile Tyr Ile Ser Asn Ile Arg Thr Glu
 20 25 30

<210> 207

<211> 394

<212> DNA

<213> Homo sapiens

<400> 207

agtctggccg cgctcttcga ctgctgctgc cactgccccg ggggtgccga gccggcgggg 60
 ggtgaggtgg ctgcgccggc ggccgggcta ggaggtgctg gactggggg cgccgggaggg 120
 gacgtggcag gccccgcggg ggccacggcg atcccagggg ccaggaaggt cccgctgcgg 180
 gcacgcaatc tgcctccgtc cttcttcacg gagccgtccc gggcaggcgg cgggcgtgtg 240
 gcccgctggg gccggacgtg agcttggggc acctggagaa gggcgcgag gccgtggagt 300
 tctttgagct gctggggccc gactacggcg ccggcacgga ggcgggagtc ttgcttgccg 360
 ccgagcctct cgacgggttc cccgccggag cctt 394

<210> 208

<211> 86

<212> PRT

<213> Homo sapiens

<400> 208

Ser Leu Ala Ala Leu Phe Asp Ser Leu Arg His Val Pro Gly Gly Ala
 1 5 10 15

Glu Pro Ala Gly Gly Glu Val Ala Ala Pro Ala Ala Gly Leu Gly Gly
 20 25 30

Ala Gly Thr Gly Gly Ala Gly Gly Asp Val Ala Gly Pro Ala Gly Ala
 35 40 45

Thr Ala Ile Pro Gly Ala Arg Lys Val Pro Leu Arg Ala Arg Asn Leu
 50 55 60

Pro Pro Ser Phe Phe Thr Glu Pro Ser Arg Ala Gly Gly Gly Arg Val
 65 70 75 80

Ala Arg Arg Gly Arg Thr
85

<210> 209
<211> 430
<212> DNA
<213> Homo sapiens

<400> 209
atgatcgctt tggagtcgat tcgacttttt tttttttttt tttttttttt taagagacag 60
agtcccaatc agtcacccag gctagagtgc agtgggtataa gcatggcaca ttgtaacctc 120
caactcctgg cctcaactga tcctcttgcc tcaggctcct gagtagctgg gactataggc 180
acatacgatc atgcctggct aatttttaat ttttttagag atgggatctc gctatgttgc 240
ccaggctggg ctcaaaactcc tggcccggag cagtcatcct gcctcagcct cccaaagcgc 300
taggattaca ggcccaagcc actgtgcctg gtcaggtgtc tttgagagtg gtgctatccc 360
actgaactgg tgagaaagt gagtagaacc aaagaaagaa aacttgatag aagcaagaat 420
tatgattgcg 430

<210> 210
<211> 53
<212> PRT
<213> Homo sapiens

<400> 210

Met Ile Ala Leu Glu Ser Ile Arg Leu Phe Phe Phe Phe Phe Phe Phe
1 5 10 15

Phe Lys Arg Gln Ser Pro Asn Gln Ser Pro Arg Leu Glu Cys Ser Gly
20 25 30

Ile Ser Met Ala His Cys Asn Leu Gln Leu Leu Ala Ser Thr Asp Pro
35 40 45

Leu Ala Ser Gly Ser
50

<210> 211
<211> 411
<212> DNA
<213> Homo sapiens

<400> 211
 gagaagagac agaaggggta ctagctaagt ttttggaag tcaaaaatta tacaaaaatt 60
 tctgactgtg caggggtcag tgagtctaac cgctgcacta ttgaagggtc aactgtactt 120
 gaaaaaagtc actttagtagca ggaagaatag catgggaaaa gattcaagac cacatagtta 180
 agtctcagat ttctagctgg tgcatacatc aactgcctct tctcaacata caccctgcaa 240
 atcctttatt ccagatcctt tttgtgaaaa atcaaaactat tattccctat gataagatct 300
 aaaagaactg acagatgtta ctctatacta acaattccat tttcaciaag aagcatctct 360
 gagttagtaa aaaaaaaaaa aaaaaaaaaa gaggaaaagt cgtatcgatg t 411

<210> 212
 <211> 41
 <212> PRT
 <213> Homo sapiens

<400> 212

Met Ile Arg Ser Lys Arg Thr Asp Arg Cys Tyr Ser Ile Leu Thr Ile
 1 5 10 15

Pro Phe Ser Gln Arg Ser Ile Ser Glu Leu Val Lys Lys Lys Lys Lys
 20 25 30

Lys Lys Glu Glu Lys Ser Tyr Arg Cys
 35 40

<210> 213
 <211> 161
 <212> DNA
 <213> Homo sapiens

<400> 213
 gcctactact actatacggc tgcgagatga cgacagaagg gctcattatt ccatatTTTT 60
 ccaccacctt cttcccaaag gcacgtgtac ctgcctgacc tcctctgcct gagaagggt 120
 cagaacaaag taaaaaaaaa aaaaaaaaaa agtcgtatcg a 161

<210> 214
 <211> 36
 <212> PRT
 <213> Homo sapiens

<400> 214

Pro Thr Thr Thr Ile Arg Leu Arg Asp Asp Asp Arg Arg Ala His Tyr

<213> Homo sapiens

<400> 217

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catcatcatc atgacgcgc gacatcgata cgactttttt tttttttttt ttttaggtaa      60
gagaaaaatct gaaaatgaga cgtttcattc acctccatat ctttactgct cagacacatt    120
ggctgatatc tgcttggtt tacttccagt gctttctcta attgcagagg catgtgaagg      180
ccgtaatctt tagaagagcc ttcaaagcct tgcattgtct ggccctgcct gtctttccag    240
cctcaccctt gtgaccgtct ccccttctgt cgtcttctcg cagc                      284
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<210> 218

<211> 60

<212> PRT

<213> Homo sapiens

<400> 218

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Met Ile Ala Arg His Arg Tyr Asp Phe Phe Phe Phe Phe Phe Leu Gly
1           5           10           15
```

```
Lys Arg Lys Ser Glu Asn Glu Thr Phe His Ser Pro Pro Tyr Leu Tyr
          20           25           30
```

```
Cys Ser Asp Thr Leu Ala Asp Ile Cys Leu Ala Leu Leu Pro Val Leu
          35           40           45
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Ser Leu Ile Ala Glu Ala Cys Glu Gly Arg Asn Leu
          50           55           60
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<210> 219

<211> 265

<212> DNA

<213> Homo sapiens

<400> 219

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gagaagacga cagaaggggt ctccaggcct cagactgtgg agctttcacg ctgcacaaac      60
ctcacagact gtgcctgatt tatggatgac attttaatta agatgttaca tctaacttta    120
aagaaaagta gttatttaga accatttgtt atgtttaaag cacggtacaa atatagcaca    180
tttcccaaac caaagaacag tgcattgcag gaaaaaatag cagctcgcaa aaaaaaaaaa    240
aaaaaaaaaa aaaaagtcgt atcga                      265
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<210> 220

<211> 60

<212> PRT
 <213> Homo sapiens

<400> 220

Met Asp Asp Ile Leu Ile Lys Met Leu His Leu Thr Leu Lys Lys Ser
 1 5 10 15

Ser Tyr Leu Glu Pro Leu Cys Met Phe Lys Ala Arg Tyr Lys Tyr Ser
 20 25 30

Thr Phe Pro Lys Pro Lys Asn Ser Ala Leu Gln Glu Lys Ile Ala Ala
 35 40 45

Arg Lys Lys Lys Lys Lys Lys Lys Lys Lys Val Val
 50 55 60

<210> 221
 <211> 291
 <212> DNA
 <213> Homo sapiens

<400> 221

catcatcatc atcatgatcg ctgcacatcg atacgacttt tttttttttt ttttttaaatt 60
 aaagacaggg ttccaccctg ttggccagga tggctcttgaa ctctgactt caggctcgccc 120
 tcctgccttg gctcccaaaa gtgctgggat tacagacgtg agccaccgca cccagcctgt 180
 ttagtgtttg atgcatagta ttttttagat ggctattgaa tgcattgaaa tgcgtacata 240
 atctttttta atctcgttct tccatctgcc cttctgtcgt cttctgcag c 291

<210> 222
 <211> 32
 <212> PRT
 <213> Homo sapiens

<400> 222

His His His His His Asp Arg Ser Thr Ser Ile Arg Leu Phe Phe Phe
 1 5 10 15

Phe Phe Leu Asn Lys Asp Arg Val Ser Pro Cys Trp Pro Gly Trp Ser
 20 25 30

<210> 223
 <211> 216
 <212> DNA

<213> Homo sapiens

<400> 223

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gaaagacgac agaaggggaag agtgggtctgg gaaggcctct gtaaggaagt agcattttaa      60
tagagtgaaa aactcagtaa cctagagcag cagcgtccaa tagaaataca atgtgaggcc      120
aggcgcggtg gctcacatct gtaatctcag cactttggga gggcgacaag agtgaaactg      180
gctctcaaaa aaaaaaaaaa aaaaaagtcg tatcga                                216

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<210> 224

<211> 20

<212> PRT

<213> Homo sapiens

<400> 224

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Glu Arg Arg Gln Lys Gly Arg Val Val Trp Glu Gly Leu Cys Lys Glu
1           5           10           15

```

```

Val Ala Phe Lys
           20

```

<210> 225

<211> 235

<212> DNA

<213> Homo sapiens

<400> 225

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cgagaagacg acagaaggga gcaagtattt gaaaaacatt gcttggtaca cagtacctct      60
caaactgcaa gaacgtaaga aatTTTTgtt cactataaaa ttacagacct gtacaaactt      120
tttctaaaaa gtaatgtatt ctcttaaaac aatggctttt ctcttttgca aaagcacagc      180
tactttttcc tggcaaaaaa aaaaaaaaaa aaaaaaaaaa aagtcgtatc gatgt          235

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<210> 226

<211> 34

<212> PRT

<213> Homo sapiens

<400> 226

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Met Tyr Ser Leu Lys Thr Met Ala Phe Leu Phe Cys Lys Ser Thr Ala
1           5           10           15

```

```

Thr Phe Ser Trp Gln Lys Lys Lys Lys Lys Lys Lys Lys Ser Tyr
           20           25           30

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Arg Cys

<210> 227
 <211> 515
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (497)..(497)
 <223> n = unknown

<400> 227
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 ccggcgcctc tttagcaggg gagctgcaca gcagctgcca tgttgctaca aactgcatcc 120
 tgggaggcat gtccctctca ggccgtttta agagaaacac tccgaggctc gtcggaggct 180
 gccggaaccc agacagctcc atctacagcc ggtaggagcg aacagtgtcg agcgagccgc 240
 ccggcggcga cggacacgcc ctgagcccgg gccagcccgt cgtggagccc gggccgaacc 300
 gccggggcct cccaccctcc aggaccctcc ggcctctcac ctgggggtct cgctgccc 360
 ggcaccctcg ggcgaggccg ggaggcgcgc gggcggaggc gcagtcggag cgcgagccc 420
 aggcgacgtg ccggggtctg gaggcggctt gattggctcc gacagccttc ctcccgccga 480
 tccctgcgc ctctcanacc cagaaccgg gtcgt 515

<210> 228
 <211> 168
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC FEATURE
 <222> (163)..(163)
 <223> X = unknown

<400> 228

Leu Gly Pro Gln Leu Arg Pro Arg Pro Arg Leu Arg Ala Ala Leu Pro
 1 5 10 15

Ser Arg Arg Leu Phe Ser Arg Gly Ala Ala Gln Gln Leu Pro Cys Cys
 20 25 30

Tyr Lys Leu His Pro Gly Arg His Val Pro Leu Arg Pro Phe Lys Glu
 35 40 45

Lys His Ser Glu Ala Arg Arg Arg Leu Pro Glu Pro Arg Gln Leu His
 50 55 60

Leu Gln Pro Val Gly Ala Asn Ser Val Glu Arg Ala Ala Arg Arg Arg
 65 70 75 80

Arg Thr Arg Pro Glu Pro Gly Pro Ala Arg Arg Gly Ala Arg Ala Glu
 85 90 95

Pro Pro Gly Pro Pro Thr Leu Gln Asp Pro Pro Ala Ser His Leu Gly
 100 105 110

Ser Ser Pro Ala Gln Ala Pro Ser Gly Glu Ala Gly Arg Arg Ala Gly
 115 120 125

Gly Gly Ala Val Gly Ala Arg Ser Pro Gly Asp Val Pro Gly Ser Gly
 130 135 140

Gly Gly Leu Ile Gly Ser Asp Ser Leu Pro Pro Ala Asp Pro Leu Arg
 145 150 155 160

Leu Ser Xaa Pro Glu Pro Gly Ser
 165

<210> 229
 <211> 311
 <212> DNA
 <213> Homo sapiens

<400> 229
 taagaaaaat tttgaatatt tttattgaat tccaatatag ttactctgaa aaaacaaatt 60
 agacagatat cctaaattga aaatcatgat gtacaaaacc cactgtcatt accaataaaa 120
 agtttaaaat aaagtgtcaa gattgatttt tacaagaaca gcattcatat atcaaaaacc 180
 tctctctttt ttataccaaa tgattaaggt atactgaaaa ttacacacct caagaaaata 240
 tatcagtaga tgaaatatta tcaactgaaga tagtcacata aggcatgatt gttttgggaa 300
 tttaaataaa a 311

<210> 230

<211> 248
 <212> DNA
 <213> Homo sapiens

<400> 230
 gagaagacga cagaagggtt atttggtgct ggagctctcc aaattaagaa tgggcagtga 60
 caaactttga acaggtaaca aacaataaat tcaaagtata tttaggatta aacagtcaat 120
 ttctaaatgg gagtctatca tgtctccctt ttgcaatact ggcttcccaa caggaattct 180
 atacttgtcc agtccaccat aatgggtatt ctcatataaa aaaaaaaaaa aaaaaaagaa 240
 aaaagtcg 248

<210> 231
 <211> 40
 <212> PRT
 <213> Homo sapiens

<400> 231

Met Gly Val Tyr His Val Ser Pro Leu Gln Tyr Trp Leu Pro Asn Arg
 1 5 10 15

Asn Ser Ile Leu Val Gln Ser Thr Ile Met Gly Ile Leu Ile Lys Lys
 20 25 30

Lys Lys Lys Lys Lys Glu Lys Ser
 35 40

<210> 232
 <211> 406
 <212> DNA
 <213> Homo sapiens

<400> 232
 attttctatg gttttattgc ctaaataata agtattatta gttatttatt gttacataac 60
 aaattactcc caaacttagc acttacatca acatgogttg ctatttcagt ttctccaggt 120
 taggaatcca ggtacagatt agctggctga gggctctctc caagggtgca gttagaatag 180
 tggtcagggc agcagagcta caatcttctc gagtttcagc tgggcaggat cogcttccag 240
 gctcactcag tgggtgttgg caggattcag ttccttgtgg gttgttggat tgagggcctc 300
 agttcctcaa tggctagtgg ctggggggccc cttgagtttc ctctacatg ggcgctctata 360
 gagcagctca cagcattgaa gctagcttca ttaaacaagc tttcac 406

<210> 233
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 233

Met Arg Cys Tyr Phe Ser Phe Ser Arg Leu Gly Ile Gln Val Gln Ile
 1 5 10 15

Ser Trp Leu Arg Val Ser Leu Lys Gly Ala Val Arg Ile Val Val Arg
 20 25 30

Ala Ala Glu Leu Gln Ser Ser Arg Val Ser Ala Gly Gln Asp Pro Leu
 35 40 45

Pro Gly Ser Leu Ser Gly Cys Trp Gln Asp Ser Val Pro Cys Gly Leu
 50 55 60

Leu Asp
 65

<210> 234
 <211> 589
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (576)..(576)
 <223> n = unknown

<220>
 <221> misc_feature
 <222> (583)..(583)
 <223> n = unknown

<400> 234
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 ataagagata atttcacggt tagtctaattg tacaaattgg atttttaaaa aatgagctct 120
 atctgtgaag cccttattcc tatagaatgt gtctttttga gtttattact tattacagac 180
 tctaaaaaca acattgctgc tgattttcaa gtaagctgcc tctttctacat agcaaattagg 240
 tacacttcac ttttcctga tttttcttag ggcgtgctat tgatttttat tgttgtctga 300
 caaaataatt tatcaaaca aaggagaaa gactaaaaaa tgtatttttc cacttttctg 360

tatcatgcat aatcagcaac aaccaatata atatttggca agagtgaaca aaaataaatt 420
 tactcttgct ccttagaaat acaaggggttc ctttttagtt acacttcttt cttttacttt 480
 gtgtcattca gtttagagca attaaatctt cttttctccc tgcgtttcca gctcagcgcc 540
 cattacgttc tgtctctttc cttagtgcatt tattgnatac tgngcatag 589

<210> 235
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 235

Met Ser Ser Ile Cys Glu Ala Leu Ile Pro Ile Glu Cys Val Phe Leu
 1 5 10 15

Ser Leu Leu Leu Ile Thr Asp Ser Lys Asn Asn Ile Ala Ala Asp Phe
 20 25 30

Gln Val Ser Cys Leu Phe Tyr Ile Ala Asn Arg Tyr Thr Ser Leu Phe
 35 40 45

Pro Asp Phe Ser
 50

<210> 236
 <211> 657
 <212> DNA
 <213> Homo sapiens

<400> 236

ggcagcccgg agacagcctc cctggctggg aatgaacgca gggcagagct cggctccggg 60
 ctctctcccc agggactcac aggacgtgt gcagccccac cccccaacctc aggccgggt 120
 ttctgggact cacaagctat ggtcaggagc gagacgccga ccatggggaa aaacagattc 180
 tgtctagacc cggccgggag ctttcccgag agggctccga gacggacggc agtcgatgct 240
 acttaggggtg gacggaagga cggcgggggtt tggaagctgg gccagaaga gtgggtttgc 300
 ctgtgtcggt gtgggttctc tgatggggac acagaactgt ggggtcccg gcagtaactc 360
 gagcccgcg acagacaggc atgtgtgggg gctgcggcac caggctgggc agcatctcag 420
 gaagcaagtg agtacctgtg cttgggttcca aggcggccat gaacttacct cactgttcag 480
 gaaacagtag aggacggcca ccaccaggcc ctgcaatgag aagagatggt caggcaggac 540

ccgcgctcgg gggagggcgg ccgcctccgc acacctacct ggaacgaccc gaggcacagc 600
 tcaaacagta tctggtatct ggaggagatg ctgatgggaa acacggcaaa caccatg 657

<210> 237
 <211> 438
 <212> PRT
 <213> Homo sapiens

<400> 237

Met Arg Thr Leu Leu Pro Pro Ala Leu Leu Thr Cys Trp Leu Leu Ala
 1 5 10 15

Pro Val Asn Ser Ile His Pro Glu Cys Arg Phe His Leu Glu Ile Gln
 20 25 30

Glu Glu Glu Thr Lys Cys Thr Glu Leu Leu Arg Ser Gln Thr Glu Lys
 35 40 45

His Lys Ala Cys Ser Gly Val Trp Asp Asn Ile Thr Cys Trp Arg Pro
 50 55 60

Ala Asn Val Gly Glu Thr Val Thr Val Pro Cys Pro Lys Val Phe Ser
 65 70 75 80

Asn Phe Tyr Ser Lys Ala Gly Asn Ile Ser Lys Asn Cys Thr Ser Asp
 85 90 95

Gly Trp Ser Glu Thr Phe Pro Asp Phe Val Asp Ala Cys Gly Tyr Ser
 100 105 110

Asp Pro Glu Asp Glu Ser Lys Ile Thr Phe Tyr Ile Leu Val Lys Ala
 115 120 125

Ile Tyr Thr Leu Gly Tyr Ser Val Ser Leu Met Ser Leu Ala Thr Gly
 130 135 140

Ser Ile Ile Leu Cys Leu Phe Arg Lys Leu His Cys Thr Arg Asn Tyr
 145 150 155 160

Ile His Leu Asn Leu Phe Leu Ser Phe Ile Leu Arg Ala Ile Ser Val
 165 170 175

Leu Val Lys Asp Asp Val Leu Tyr Ser Ser Ser Gly Thr Leu His Cys
 180 185 190
 Pro Asp Gln Pro Ser Ser Trp Val Gly Cys Lys Leu Ser Leu Val Phe
 195 200 205
 Leu Gln Tyr Cys Ile Met Ala Asn Phe Phe Trp Leu Leu Val Glu Gly
 210 215 220
 Leu Tyr Leu His Thr Leu Leu Val Ala Met Leu Pro Pro Arg Arg Cys
 225 230 235 240
 Phe Leu Ala Tyr Leu Leu Ile Gly Trp Gly Leu Pro Thr Val Cys Ile
 245 250 255
 Gly Ala Trp Thr Ala Ala Arg Leu Tyr Leu Glu Asp Thr Gly Cys Trp
 260 265 270
 Asp Thr Asn Asp His Ser Val Pro Trp Trp Val Ile Arg Ile Pro Ile
 275 280 285
 Leu Ile Ser Ile Ile Val Asn Phe Val Leu Phe Ile Ser Ile Ile Arg
 290 295 300
 Ile Leu Leu Gln Lys Leu Thr Ser Pro Asp Val Gly Gly Asn Asp Gln
 305 310 315 320
 Ser Gln Tyr Lys Arg Leu Ala Lys Ser Thr Leu Leu Leu Ile Pro Leu
 325 330 335
 Phe Gly Val His Tyr Met Val Phe Ala Val Phe Pro Ile Ser Ile Ser
 340 345 350
 Ser Lys Tyr Gln Ile Leu Phe Glu Leu Cys Leu Gly Ser Phe Gln Gly
 355 360 365
 Leu Val Val Ala Val Leu Tyr Cys Phe Leu Asn Ser Glu Val Gln Cys
 370 375 380
 Glu Leu Lys Arg Lys Trp Arg Ser Arg Cys Pro Thr Pro Ser Ala Ser
 385 390 395 400

Arg Asp Tyr Arg Val Cys Gly Ser Ser Phe Ser His Asn Gly Ser Glu
 405 410 415

Gly Ala Leu Gln Phe His Arg Ala Ser Arg Ala Gln Ser Phe Leu Gln
 420 425 430

Thr Glu Thr Ser Val Ile
 435

<210> 238
 <211> 1750
 <212> DNA
 <213> Homo sapiens

<400> 238
 gcggtcttat ataagccaga tccgcagggg agtccgcaga aggggttaaag aggtctttgg 60
 gcttcggcga cctcgcccg cgcagaaacc ggtaagaaga cagtgggctg cgcgtctcat 120
 tttcagcctt gcccggactc tcccaaagcc ggcgcccagt agtgggtcca gagcccacag 180
 gtggcccccg gcagtctctg gggcgcatgg agcggcggtta atagggctgg cggcgccaggc 240
 cagtagccgc tccaacatga acctcgtggg cagctacgca caccatcacc accatcacca 300
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<210> 239
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 239

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His Pro Ala His Pro Met Leu His Glu Pro Phe Leu Phe Gly Pro Ala
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Ser Arg Cys His Gln Glu Arg Pro Tyr Phe Gln Ser Trp Leu Leu Ser
 35 40 45

Pro Ala Asp Ala Ala Pro Asp Phe Pro Ala Gly Gly Pro Pro Pro Ala
 50 55 60

Ala Ala Ala Ala Ala Thr Ala Tyr Gly Pro Asp Ala Arg Pro Gly Gln
 65 70 75 80

Ser Pro Gly Arg Leu Glu Ala Leu Gly Gly Arg Leu Gly Arg Arg Lys
 85 90 95

Gly Ser Gly Pro Lys Lys Glu Arg Arg Arg Thr Glu Ser Ile Asn Ser
 100 105 110

Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn Val Pro Ala Asp Thr
115 120 125

Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala Thr Ser Tyr Ile Ala
130 135 140

Tyr Leu Met Asp Val Leu Ala Lys Asp Ala Gln Ser Gly Asp Pro Glu
145 150 155 160

Ala Phe Lys Ala Glu Leu Lys Lys Ala Asp Gly Gly Arg Glu Ser Lys
165 170 175

Arg Lys Arg Glu Leu Gln Gln His Glu Gly Phe Pro Pro Ala Leu Gly
180 185 190

Pro Val Glu Lys Arg Ile Lys Gly Arg Thr Gly Trp Pro Gln Gln Val
195 200 205

Trp Ala Leu Glu Leu Asn Gln
210 215

<210> 240
<211> 489
<212> DNA
<213> Homo sapiens

<400> 240
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<210> 241
<211> 47

<212> PRT
 <213> Homo sapiens

<400> 241

Met Ala Asp Met Glu Val Gly Glu Ser Glu Leu Pro Glu Asn Leu Gly
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Lys Ser Asn Lys Leu Leu Val Ser Thr Lys Ser Val Phe Ser Ser Gln
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Arg Val Lys Gly Ala Ile Trp Glu Gln Arg Ser Ile Leu Lys Leu
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<210> 242
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 <212> DNA
 <213> Homo sapiens

<400> 242

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<210> 243
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 243

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His Leu Trp Asn Pro Gln Ser Ser Thr His Lys Thr Asp Gly Val Ser
20 25 30

Leu Trp Ala Gly Arg Gly Glu Ala Arg His Ser Ala Ser Leu Trp Lys
35 40 45

Pro Arg Gln Arg Leu Ser Lys Pro His Ser Tyr Ala Gln Ser Leu Ile
50 55 60

Pro Phe Leu Glu Leu Glu Leu Met Pro Ser Val Ala Leu Gly Phe Ser
65 70 75 80

Pro Phe Gly Ser Phe Asp Arg Arg Asn Pro Thr Gln Arg Leu Ala Ala
85 90 95

Ala Glu Asp

<210> 244

<211> 2114

<212> DNA

<213> Homo sapiens

<400> 244

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<210> 245

<211> 628

<212> PRT

<213> Homo sapiens

<400> 245

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Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val His Pro Ala
 20 25 30

Arg Thr Leu Ala Gly Glu Thr Gly Thr Glu Ser Ala Pro Leu Gly Gly
 35 40 45

Val Leu Thr Thr Pro His Asn Ile Ser Ser Leu Ser Pro Arg Gln Leu
 50 55 60

Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu Arg Val
 65 70 75 80

Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu Ser Thr
 85 90 95

Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro Glu Asp
 100 105 110

Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro Asp Ala
 115 120 125

Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile Thr Lys
 130 135 140

Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln Arg Leu
 145 150 155 160

Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu Leu Ser
 165 170 175

Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu Pro Gly
 180 185 190

Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu Val Ser
 195 200 205

Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg Ala Ala
 210 215 220
 Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp Ser Val
 225 230 235 240
 Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly Gln Pro
 245 250 255
 Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg Gln Arg
 260 265 270
 Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile Leu Arg
 275 280 285
 Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser Gly Lys
 290 295 300
 Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys Trp Glu
 305 310 315 320
 Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met Asp Arg
 325 330 335
 Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu Lys His
 340 345 350
 Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val Ile Gln
 355 360 365
 His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile Arg Lys
 370 375 380
 Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu Val Asp
 385 390 395 400
 Lys Gly His Glu Met Ser Pro Gln Ala Pro Arg Arg Pro Leu Pro Gln
 405 410 415
 Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln Leu Asp
 420 425 430

Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys
 435 440 445
 Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser Ile Trp
 450 455 460
 Ala Val Arg Pro Gln Asp Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp
 465 470 475 480
 Val Leu Tyr Pro Lys Ala Arg Leu Ala Phe Gln Asn Met Asn Gly Ser
 485 490 495
 Glu Tyr Phe Val Lys Ile Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu
 500 505 510
 Asp Leu Lys Ala Leu Ser Gln Gln Asn Val Ser Met Asp Leu Ala Thr
 515 520 525
 Phe Met Lys Leu Arg Thr Asp Ala Val Leu Pro Leu Thr Val Ala Glu
 530 535 540
 Val Gln Lys Leu Leu Gly Pro His Val Glu Gly Leu Lys Ala Glu Glu
 545 550 555 560
 Arg His Arg Pro Val Arg Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp
 565 570 575
 Leu Asp Thr Leu Gly Leu Gly Leu Gln Gly Gly Ile Pro Asn Gly Tyr
 580 585 590
 Leu Val Leu Asp Leu Ser Val Gln Glu Thr Leu Ser Gly Thr Pro Cys
 595 600 605
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 Ser Thr Leu Ala
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 <211> 537
 <212> DNA
 <213> Homo sapiens

<400> 246
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 cccaggcccc tcagctctgt gagccctcct gacttcgatt cctcctctgc ttgcactctt 480
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<210> 247
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 247

Met Arg Trp Thr Phe Phe Tyr Arg Arg Gly Ile Cys Ser Ser Ile Lys
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Leu Ser Thr Leu Ser Arg Leu Asp Pro Asn Pro Gly Ser Leu Thr Pro
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Lys Pro Cys Met His Val Tyr Ile Thr Pro Gln Ala Pro Gln Leu Cys
 35 40 45

Glu Pro Ser
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<210> 248
 <211> 414
 <212> DNA
 <213> Homo sapiens

<400> 248
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<210> 249
 <211> 21
 <212> PRT
 <213> Homo sapiens

<400> 249

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Leu Leu Phe Ser Phe
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<210> 250
 <211> 1584
 <212> DNA
 <213> Homo sapiens

<400> 250
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<210> 251
<211> 474
<212> PRT
<213> Homo sapiens

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<400> 251

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Met Ala Leu Ala Val Ala Pro Trp Gly Arg Gln Trp Glu Glu Ala Arg
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Ala Leu Gly Arg Ala Val Arg Met Leu Gln Arg Leu Glu Glu Gln Cys
20           25           30

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```

Val Asp Pro Arg Leu Ser Val Ser Pro Pro Ser Leu Arg Asp Leu Leu
35           40           45

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```

Pro Arg Thr Ala Gln Leu Leu Arg Glu Val Ala His Ser Arg Arg Ala
50           55           60

```

```

Ala Gly Gly Gly Gly Pro Gly Gly Pro Gly Gly Ser Gly Asp Phe Leu
65           70           75           80

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Leu Ile Tyr Leu Ala Asn Leu Glu Ala Lys Ser Arg Gln Val Ala Ala
85           90           95

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Leu Leu Pro Pro Arg Gly Arg Arg Ser Ala Asn Asp Glu Leu Phe Arg
 100 105 110

Ala Gly Ser Arg Leu Arg Arg Gln Leu Ala Lys Leu Ala Ile Ile Phe
 115 120 125

Ser His Met His Ala Glu Leu His Ala Leu Phe Pro Gly Gly Lys Tyr
 130 135 140

Cys Gly His Met Tyr Gln Leu Thr Lys Ala Pro Ala His Thr Phe Trp
 145 150 155 160

Arg Glu Ser Cys Gly Ala Arg Cys Val Leu Pro Trp Ala Glu Phe Glu
 165 170 175

Ser Leu Leu Gly Thr Cys His Pro Val Glu Pro Gly Cys Thr Ala Leu
 180 185 190

Ala Leu Arg Thr Thr Ile Asp Leu Thr Cys Ser Gly His Val Ser Ile
 195 200 205

Phe Glu Phe Asp Val Phe Thr Arg Leu Phe Gln Pro Trp Pro Thr Leu
 210 215 220

Leu Lys Asn Trp Gln Leu Leu Ala Val Asn His Pro Gly Tyr Met Ala
 225 230 235 240

Phe Leu Thr Tyr Asp Glu Val Gln Glu Arg Leu Gln Ala Cys Arg Asp
 245 250 255

Lys Pro Gly Ser Tyr Ile Phe Arg Pro Ser Cys Thr Arg Leu Gly Gln
 260 265 270

Trp Ala Ile Gly Tyr Val Ser Ser Asp Gly Ser Ile Leu Gln Thr Ile
 275 280 285

Pro Ala Asn Lys Pro Leu Ser Gln Val Leu Leu Glu Gly Gln Lys Asp
 290 295 300

Gly Phe Tyr Leu Tyr Pro Asp Gly Lys Thr His Asn Pro Asp Leu Thr
 305 310 315 320

Glu Leu Gly Gln Ala Glu Pro Gln Gln Arg Ile His Val Ser Glu Glu
325 330 335

Gln Leu Gln Leu Tyr Trp Ala Met Asp Ser Thr Phe Glu Leu Cys Lys
340 345 350

Ile Cys Ala Glu Ser Asn Lys Asp Val Lys Ile Glu Pro Cys Gly His
355 360 365

Leu Leu Cys Ser Cys Cys Leu Ala Ala Trp Gln His Ser Asp Ser Gln
370 375 380

Thr Cys Pro Phe Cys Arg Cys Glu Ile Lys Gly Trp Glu Ala Val Ser
385 390 395 400

Ile Tyr Gln Phe Tyr Gly Gln Ala Thr Ala Glu Asp Ser Gly Asn Ser
405 410 415

Ser Asp Gln Glu Gly Arg Glu Leu Glu Leu Gly Gln Val Pro Leu Ser
420 425 430

Ala Pro Pro Leu Pro Pro Arg Pro Asp Leu Pro Pro Arg Lys Pro Arg
435 440 445

Asn Ala Gln Pro Lys Val Arg Leu Leu Lys Gly Asn Ser Pro Pro Ala
450 455 460

Ala Leu Gly Pro Gln Asp Pro Ala Pro Ala
465 470

<210> 252

<211> 454

<212> DNA

<213> Homo sapiens

<400> 252

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actttactga gaggcacctg gggttccaga gaaagtcttc tagctggggg cctcctgagg	180
acaaccctgc tcccatttgg cctggatttg ggggtcccttc ctccctccatg gtccatttag	240
gccatgttgt gtgtcagtac gacctacacg tgaactccag aggaaaggcc tgcccgggat	300

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gttgctgttg ttctgataca gaaacaattg gatgccctta aacgcacatg ccttcccatg 360
taatgtcttg gcaaagtgga aatgagcact cagaattgtc gctggcagga gtgctgctgg 420
gttcgcgttt ctttatgcaa tgtgccatca gtca 454

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<210> 253
<211> 37
<212> PRT
<213> Homo sapiens

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<400> 253

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Met Val His Leu Gly His Val Val Cys Gln Tyr Asp Leu His Val Asn
1          5          10          15

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Ser Arg Gly Lys Ala Cys Pro Gly Cys Cys Cys Cys Ser Asp Thr Glu
          20          25          30

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Thr Ile Gly Cys Pro
          35

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<210> 254
<211> 588
<212> DNA
<213> Homo sapiens

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<220>
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<222> (405)..(405)
<223> n = unknown

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<220>
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<222> (564)..(564)
<223> n = unknown

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taaaaaagcc cggtttttaa aacctaaaac ctaaaaccgg cccccccaa aaaaaaacc 180
caagggggcc cccaaaacat tccccttccc ttgggagggg ttaccgaggc ttggttatca 240
taaccagcc ttttccccca aaactaaagg ggccaatgga acaaaacggt ttggaaccgg 300
tcctcccccc ccgataaaa aggggggggg ggggttttgg ggaaaaaatt cattaaccct 360

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tctgaccttt tggggcaaac tggggggccct ggccagcccc agaanccttt tggggccacgg 420
 tttggaggac cccacccgaa acggttggtt taatataccg aacaagaaag cggcccaagg 480
 ggggatggtt ggagaagctc tcaacacaca gggcctggcc aggaccata tcacaagggg 540
 agtattcccc agcttaaaaa attnggggcc tttttccgct ttttacca 588

<210> 255
 <211> 75
 <212> PRT
 <213> Homo sapiens

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 <223> X = unknown

<220>
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 <222> (68)..(68)
 <223> X = unknown

<400> 255

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 1 5 10 15

Leu Gly His Gly Leu Glu Asp Pro Thr Arg Asn Gly Trp Phe Asn Ile
 20 25 30

Pro Asn Lys Lys Ala Pro Gln Gly Gly Met Val Gly Glu Ala Leu Asn
 35 40 45

Thr Gln Gly Leu Ala Arg Thr His Ile Thr Arg Gly Val Phe Pro Ser
 50 55 60

Leu Lys Asn Xaa Gly Pro Phe Ser Ala Phe Tyr
 65 70 75

<210> 256
 <211> 996
 <212> DNA
 <213> Homo sapiens

<400> 256
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cccctgggag acctggcagg cctggagggtg tgagtcggct ctgagcagct gctctgggag 240
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ccaaatctca tctttagctt ccataatcc tcccatgttg tgggagggac ccagtgggag 720
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<210> 257
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 257

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Met Gly Leu Thr Arg Ser Asp Gly Val Lys Asn Gly Ser Phe Ser Ala
1           5           10           15

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```

Gln Ala Leu Cys Leu Leu Pro Phe Thr Lys Asp Val Thr Cys Phe Ser
20           25           30

```

```

Leu Pro Ser Ala Met Ile Val Arg Pro Pro
35           40

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<210> 258
 <211> 560
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
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 <223> n = unknown

<400> 258
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 gtgtctgtac aggggtttga tttctttccc ttgtataact acacaacaat cctacagtgt 180
 aacatatgga atcattttga atagacttgt gtgctataag ctttcagcag gtcctctgtc 240
 tctagaataa gcatgttggt tattttcaga taatcagaaa taagtgtgct gacaagctgg 300
 acacaatctg ggtgtgccca gcttaccttt ctttctgatg tttaaattga aggctgcagc 360
 caatggaata tggtcagctg gttttccttg gcttcctaga ttaaaaaaaaa ataataaagc 420
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<210> 259
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 259

Met Lys Met Leu Asn Ser Ser Val Ser Thr Trp His Phe Lys Ser Asp
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Ile Arg Cys Leu Tyr Arg Val Leu Ile Ser Phe Pro Cys Ile Thr Thr
 20 25 30

Gln Gln Ser Tyr Ser Val Thr Tyr Gly Ile Ile Leu Asn Arg Leu Val
 35 40 45

Cys Tyr Lys Leu Ser Ala Gly Pro Leu Ser Leu Glu
 50 55 60

<210> 260
 <211> 4834
 <212> DNA
 <213> Homo sapiens

<400> 260
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 aacgcaataa ggatagaaat agtagtgtac accggtaaag aagggaagaa ctctcatggg 240
 tgtccaattg ctaagtgggt tttaagaaga agcagtgtatg aagaaaaagt tctttgtttg 300
 gtccggcagc gtacaggcca ccaactgtcca actgctgtga tgggtgggtgct catcatgggtg 360
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 aagtcataca atgggcaccc taccgacaga agatgcaccc tcaatgaaaa tcgtacctgt 480
 acatgtcaag gaattgatcc agagacttgt ggagcttcat tctcttttgg ctgttcatgg 540
 agtatgtact ttaatggctg taagtttgggt agaagcccaa gcccagaag atttagaatt 600
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 cgattagctc caatttataa gcagtatgct ccagtagctt accaaaatca ggtggaatat 720
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acagatatatt gtactgaagt ctgatacaga attagaaaaa aaaaattctt gttgaaatat	3360

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<210> 261
<211> 735
<212> PRT
<213> Homo sapiens

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<400> 261

Phe Phe Thr Asn Pro Thr Lys Asn Leu Val Ser Ile Thr Lys Asp Ser
1 5 10 15

Glu Leu Pro Thr Cys Ser Cys Leu Asp Arg Val Ile Gln Lys Asp Lys
20 25 30

Gly Pro Tyr Tyr Thr His Leu Gly Ala Gly Pro Ser Val Ala Ala Val
35 40 45

Arg Glu Ile Met Glu Asn Arg Tyr Gly Gln Lys Gly Asn Ala Ile Arg
50 55 60

Ile Glu Ile Val Val Tyr Thr Gly Lys Glu Gly Lys Ser Ser His Gly
65 70 75 80

Cys Pro Ile Ala Lys Trp Val Leu Arg Arg Ser Ser Asp Glu Glu Lys
85 90 95

Val Leu Cys Leu Val Arg Gln Arg Thr Gly His His Cys Pro Thr Ala
100 105 110

Val Met Val Val Leu Ile Met Val Trp Asp Gly Ile Pro Leu Pro Met
115 120 125

Ala Asp Arg Leu Tyr Thr Glu Leu Thr Glu Asn Leu Lys Ser Tyr Asn
130 135 140

Gly His Pro Thr Asp Arg Arg Cys Thr Leu Asn Glu Asn Arg Thr Cys
145 150 155 160

Thr Cys Gln Gly Ile Asp Pro Glu Thr Cys Gly Ala Ser Phe Ser Phe
165 170 175

Gly Cys Ser Trp Ser Met Tyr Phe Asn Gly Cys Lys Phe Gly Arg Ser
180 185 190

Pro Ser Pro Arg Arg Phe Arg Ile Asp Pro Ser Ser Pro Leu His Glu
195 200 205

Lys Asn Leu Glu Asp Asn Leu Gln Ser Leu Ala Thr Arg Leu Ala Pro
210 215 220

Ile Tyr Lys Gln Tyr Ala Pro Val Ala Tyr Gln Asn Gln Val Glu Tyr
225 230 235 240

Glu Asn Val Ala Arg Glu Cys Arg Leu Gly Ser Lys Glu Gly Arg Pro
245 250 255

Phe Ser Gly Val Thr Ala Cys Leu Asp Phe Cys Ala His Pro His Arg
260 265 270

Asp Ile His Asn Met Asn Asn Gly Ser Thr Val Val Cys Thr Leu Thr
275 280 285

Arg Glu Asp Asn Arg Ser Leu Gly Val Ile Pro Gln Asp Glu Gln Leu
290 295 300

His Val Leu Pro Leu Tyr Lys Leu Ser Asp Thr Asp Glu Phe Gly Ser
305 310 315 320

Lys Glu Gly Met Glu Ala Lys Ile Lys Ser Gly Ala Ile Glu Val Leu
325 330 335

Ala Pro Arg Arg Lys Lys Arg Thr Cys Phe Thr Gln Pro Val Pro Arg
340 345 350

Ser Gly Lys Lys Arg Ala Ala Met Met Thr Glu Val Leu Ala His Lys
355 360 365

Ile Arg Ala Val Glu Lys Lys Pro Ile Pro Arg Ile Lys Arg Lys Asn
370 375 380

Asn Ser Thr Thr Thr Asn Asn Ser Lys Pro Ser Ser Leu Pro Thr Leu
385 390 395 400

Gly Ser Asn Thr Glu Thr Val Gln Pro Glu Val Lys Ser Glu Thr Glu
405 410 415

Pro His Phe Ile Leu Lys Ser Ser Asp Asn Thr Lys Thr Tyr Ser Leu
420 425 430

Met Pro Ser Ala Pro His Pro Val Lys Glu Ala Ser Pro Gly Phe Ser
435 440 445

Trp Ser Pro Lys Thr Ala Ser Ala Thr Pro Ala Pro Leu Lys Asn Asp
 450 455 460

Ala Thr Ala Ser Cys Gly Phe Ser Glu Arg Ser Ser Thr Pro His Cys
 465 470 475 480

Thr Met Pro Ser Gly Arg Leu Ser Gly Ala Asn Ala Ala Ala Ala Asp
 485 490 495

Gly Pro Gly Ile Ser Gln Leu Gly Glu Val Ala Pro Leu Pro Thr Leu
 500 505 510

Ser Ala Pro Val Met Glu Pro Leu Ile Asn Ser Glu Pro Ser Thr Gly
 515 520 525

Val Thr Glu Pro Leu Thr Pro His Gln Pro Asn His Gln Pro Ser Phe
 530 535 540

Leu Thr Ser Pro Gln Asp Leu Ala Ser Ser Pro Met Glu Glu Asp Glu
 545 550 555 560

Gln His Ser Glu Ala Asp Glu Pro Pro Ser Asp Glu Pro Leu Ser Asp
 565 570 575

Asp Pro Leu Ser Pro Ala Glu Glu Lys Leu Pro His Ile Asp Glu Tyr
 580 585 590

Trp Ser Asp Ser Glu His Ile Phe Leu Asp Ala Asn Ile Gly Gly Val
 595 600 605

Ala Ile Ala Pro Ala His Gly Ser Val Leu Ile Glu Cys Ala Arg Arg
 610 615 620

Glu Leu His Ala Thr Thr Pro Val Glu His Pro Asn Arg Asn His Pro
 625 630 635 640

Thr Arg Leu Ser Leu Val Phe Tyr Gln His Lys Asn Leu Asn Lys Pro
 645 650 655

Gln His Gly Phe Glu Leu Asn Lys Ile Lys Phe Glu Ala Lys Glu Ala
 660 665 670

Lys Asn Lys Lys Met Lys Ala Ser Glu Gln Lys Asp Gln Ala Ala Asn
 675 680 685

Glu Gly Pro Glu Gln Ser Ser Glu Val Asn Glu Leu Asn Gln Ile Pro
 690 695 700

Ser His Lys Ala Leu Thr Leu Thr His Asp Asn Val Val Thr Val Ser
 705 710 715 720

Pro Tyr Ala Leu Thr His Val Ala Gly Pro Tyr Asn His Trp Val
 725 730 735

<210> 262
 <211> 1155
 <212> DNA
 <213> Homo sapiens

<400> 262
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 gacccaata atctggtttt tggaactgtg ttcacggatc atatgctgac ggtggagtgg 180
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 ggagtagata ataaaattcg actgtttcag ccaaacctca acatggatag aatgtatcgc 360
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 cgtcctgcat tcattggaac tgagccttct cttggagtca agaagcctac caaagccctg 540
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<210> 263
 <211> 384
 <212> PRT
 <213> Homo sapiens

<400> 263

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Lys Glu Val Val Gly Thr Phe Lys Ala Lys Asp Leu Ile Val Thr Pro
 20 25 30

Ala Thr Ile Leu Lys Glu Lys Pro Asp Pro Asn Asn Leu Val Phe Gly
 35 40 45

Thr Val Phe Thr Asp His Met Leu Thr Val Glu Trp Ser Ser Glu Phe
 50 55 60

Gly Trp Glu Lys Pro His Ile Lys Pro Leu Gln Asn Leu Ser Leu His
 65 70 75 80

Pro Gly Ser Ser Ala Leu His Tyr Ala Val Glu Leu Phe Glu Gly Leu
 85 90 95

Lys Ala Phe Arg Gly Val Asp Asn Lys Ile Arg Leu Phe Gln Pro Asn
 100 105 110

Leu Asn Met Asp Arg Met Tyr Arg Ser Ala Val Arg Ala Thr Leu Pro
 115 120 125

Val Phe Asp Lys Glu Glu Leu Leu Glu Cys Ile Gln Gln Leu Val Lys
 130 135 140

Leu Asp Gln Glu Trp Val Pro Tyr Ser Thr Ser Ala Ser Leu Tyr Ile
 145 150 155 160

Arg Pro Ala Phe Ile Gly Thr Glu Pro Ser Leu Gly Val Lys Lys Pro
 165 170 175

Thr Lys Ala Leu Leu Phe Val Leu Leu Ser Pro Val Gly Pro Tyr Phe
180 185 190

Ser Ser Gly Thr Phe Asn Pro Val Ser Leu Trp Ala Asn Pro Lys Tyr
195 200 205

Val Arg Ala Trp Lys Gly Gly Thr Gly Asp Cys Lys Met Gly Gly Asn
210 215 220

Tyr Gly Ser Ser Leu Phe Ala Gln Cys Glu Asp Val Asp Asn Gly Cys
225 230 235 240

Gln Gln Val Leu Trp Leu Tyr Gly Arg Asp His Gln Ile Thr Glu Val
245 250 255

Gly Thr Met Asn Leu Phe Leu Tyr Trp Ile Asn Glu Asp Gly Glu Glu
260 265 270

Glu Leu Ala Thr Pro Pro Leu Asp Gly Ile Ile Leu Pro Gly Val Thr
275 280 285

Arg Arg Cys Ile Leu Asp Leu Ala His Gln Trp Gly Glu Phe Lys Val
290 295 300

Ser Glu Arg Tyr Leu Thr Met Asp Asp Leu Thr Thr Ala Leu Glu Gly
305 310 315 320

Asn Arg Val Arg Glu Met Phe Ser Ser Gly Thr Ala Cys Val Val Cys
325 330 335

Pro Val Ser Asp Ile Leu Tyr Lys Gly Glu Thr Ile His Ile Pro Thr
340 345 350

Met Glu Asn Gly Pro Lys Leu Ala Ser Arg Ile Leu Ser Lys Leu Thr
355 360 365

Asp Ile Gln Tyr Gly Arg Glu Glu Ser Asp Trp Thr Ile Val Leu Ser
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<210> 264
<211> 2732
<212> DNA

<213> Homo sapiens

<400> 264

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<210> 265

<211> 430

<212> PRT

<213> Homo sapiens

<400> 265

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Met Lys Pro Ser Leu Leu Cys Arg Pro Leu Ser Cys Phe Leu Met Leu
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Leu Pro Trp Pro Leu Ala Thr Leu Thr Ser Thr Thr Leu Trp Gln Cys
20           25           30

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Pro Pro Gly Glu Glu Pro Asp Leu Asp Pro Gly Gln Gly Thr Leu Cys
35           40           45

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Arg Pro Cys Pro Pro Gly Thr Phe Ser Ala Ala Trp Gly Ser Ser Pro
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 Cys Gln Pro His Ala Arg Cys Ser Leu Trp Arg Arg Leu Glu Ala Gln
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 Trp Phe Gly Pro Trp Gly Val Pro Arg Val Pro Cys Gln Pro Cys Ser
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 115 120 125
 Arg Arg Gly Val Glu Val Ala Ala Gly Ala Ser Ser Gly Gly Glu Thr
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 Arg Gln Pro Gly Asn Gly Thr Arg Ala Gly Gly Pro Glu Glu Thr Ala
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 Ala Gln Tyr Ala Val Ile Ala Ile Val Pro Val Phe Cys Leu Met Gly
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 Cys Thr Ala His Lys Glu Val Gly Pro Gly Pro Gly Gly Gly Ser
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 Gly Ile Asn Pro Ala Tyr Arg Thr Glu Asp Ala Asn Glu Asp Thr Ile
 210 215 220
 Gly Val Leu Val Arg Leu Ile Thr Glu Lys Lys Glu Asn Ala Ala Ala
 225 230 235 240
 Leu Glu Glu Leu Leu Lys Glu Tyr His Ser Lys Gln Leu Val Gln Thr
 245 250 255
 Ser His Arg Pro Val Ser Lys Leu Pro Pro Ala Pro Pro Asn Val Pro
 260 265 270

His Ile Cys Pro His Arg His His Leu His Thr Val Gln Gly Leu Ala
 275 280 285

Ser Leu Ser Gly Pro Cys Cys Ser Arg Cys Ser Gln Lys Lys Trp Pro
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Glu Val Leu Leu Ser Pro Glu Ala Val Ala Ala Thr Thr Pro Val Pro
 305 310 315 320

Ser Leu Leu Pro Asn Pro Thr Arg Val Pro Lys Ala Gly Ala Lys Ala
 325 330 335

Gly Arg Gln Gly Glu Ile Thr Ile Leu Ser Val Gly Arg Phe Arg Val
 340 345 350

Ala Arg Ile Pro Glu Gln Arg Thr Ser Ser Met Val Ser Glu Val Lys
 355 360 365

Thr Ile Thr Glu Ala Gly Pro Ser Trp Gly Asp Leu Pro Asp Ser Pro
 370 375 380

Gln Pro Gly Leu Pro Pro Glu Gln Gln Ala Leu Leu Gly Ser Gly Gly
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Ser Arg Thr Lys Trp Leu Lys Pro Pro Ala Glu Asn Lys Ala Glu Glu
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Asn Arg Tyr Val Val Arg Leu Ser Glu Ser Asn Leu Val Ile
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<210> 266

<211> 3696

<212> DNA

<213> Homo sapiens

<400> 266

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3696

<210> 267
 <211> 1019
 <212> PRT
 <213> Homo sapiens

<400> 267

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Ala Gly Leu Ile Ala Val Ser Cys Leu Thr Ile Lys Glu Ser Gln Arg
 35 40 45

Gly Ala Ala Leu Gly Gln Ser His Glu Ala Arg Ala Thr Phe Lys Ile
 50 55 60

Thr Ser Gly Val Thr Tyr Asn Pro Asn Leu Gln Asp Lys Leu Ser Val
 65 70 75 80

Asp Phe Lys Val Leu Ala Phe Asp Leu Gln Gln Met Ile Asp Glu Ile
 85 90 95

Phe Leu Ser Ser Asn Leu Lys Asn Glu Tyr Lys Asn Ser Arg Val Leu
 100 105 110

Gln Phe Glu Asn Gly Ser Ile Ile Val Val Phe Asp Leu Phe Phe Ala
 115 120 125

Gln Trp Val Ser Asp Gln Asn Val Lys Glu Glu Leu Ile Gln Gly Leu
 130 135 140

Glu Ala Asn Lys Ser Ser Gln Leu Val Thr Phe His Ile Asp Leu Asn
 145 150 155 160

Ser Val Asp Ile Leu Asp Lys Leu Thr Thr Thr Ser His Leu Ala Thr
 165 170 175

Pro Gly Asn Val Ser Ile Glu Cys Leu Pro Gly Ser Ser Pro Cys Thr
 180 185 190

Asp Ala Leu Thr Cys Ile Lys Ala Asp Leu Phe Cys Asp Gly Glu Val
 195 200 205
 Asn Cys Pro Asp Gly Ser Asp Glu Asp Asn Lys Met Cys Ala Thr Val
 210 215 220
 Cys Asp Gly Arg Phe Leu Leu Thr Gly Ser Ser Gly Ser Phe Gln Ala
 225 230 235 240
 Thr His Tyr Pro Lys Pro Ser Glu Thr Ser Val Val Cys Gln Trp Ile
 245 250 255
 Ile Arg Val Asn Gln Gly Leu Ser Ile Lys Leu Ser Phe Asp Asp Phe
 260 265 270
 Asn Thr Tyr Tyr Thr Asp Ile Leu Asp Ile Tyr Glu Gly Val Gly Ser
 275 280 285
 Ser Lys Ile Leu Arg Ala Ser Ile Trp Glu Thr Asn Pro Gly Thr Ile
 290 295 300
 Arg Ile Phe Ser Asn Gln Val Thr Ala Thr Phe Leu Ile Glu Ser Asp
 305 310 315 320
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 325 330 335
 Ser Glu Leu Asn Asn Tyr Glu Lys Ile Asn Cys Asn Phe Glu Asp Gly
 340 345 350
 Phe Cys Phe Trp Val Gln Asp Leu Asn Asp Asp Asn Glu Trp Glu Arg
 355 360 365
 Ile Gln Gly Ser Thr Phe Ser Pro Phe Thr Gly Pro Asn Phe Asp His
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Thr Leu Glu Pro Ala Cys Leu Ser Phe Trp Tyr His Met Tyr Gly Glu
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 Asn Val His Lys Leu Ser Ile Asn Ile Ser Asn Asp Gln Asn Met Glu
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 450 455 460
 Gly Gln Val Thr Leu Asn Glu Thr Val Lys Phe Lys Val Ala Phe Asn
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 Ala Phe Lys Asn Lys Ile Leu Ser Asp Ile Ala Leu Asp Asp Ile Ser
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 Gly Lys Asn Ile Gln Leu His Phe Gln Glu Phe Asp Leu Glu Asn Ile
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 610 615 620
 Gly Gly Phe Lys Ala Asn Phe Thr Thr Gly Tyr His Leu Gly Ile Pro
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Glu Pro Cys Lys Ala Asp His Phe Gln Cys Lys Asn Gly Glu Cys Val
645 650 655

Pro Leu Val Asn Leu Cys Asp Gly His Leu His Cys Glu Asp Gly Ser
660 665 670

Asp Glu Ala Asp Cys Val Arg Phe Phe Asn Gly Thr Thr Asn Asn Asn
675 680 685

Gly Leu Val Arg Phe Arg Ile Gln Ser Ile Trp His Thr Ala Cys Ala
690 695 700

Glu Asn Trp Thr Thr Gln Ile Ser Asn Asp Val Cys Gln Leu Leu Gly
705 710 715 720

Leu Gly Ser Gly Asn Ser Ser Lys Pro Ile Phe Ser Thr Asp Gly Gly
725 730 735

Pro Phe Val Lys Leu Asn Thr Ala Pro Asp Gly His Leu Ile Leu Thr
740 745 750

Pro Ser Gln Gln Cys Leu Gln Asp Ser Leu Ile Arg Leu Gln Cys Asn
755 760 765

His Lys Ser Cys Gly Lys Lys Leu Ala Ala Gln Asp Ile Thr Pro Lys
770 775 780

Ile Val Gly Gly Ser Asn Ala Lys Glu Gly Ala Trp Pro Trp Val Val
785 790 795 800

Gly Leu Tyr Tyr Gly Gly Arg Leu Leu Cys Gly Ala Ser Leu Val Ser
805 810 815

Ser Asp Trp Leu Val Ser Ala Ala His Cys Val Tyr Gly Arg Asn Leu
820 825 830

Glu Pro Ser Lys Trp Thr Ala Ile Leu Gly Leu His Met Lys Ser Asn
835 840 845

Leu Thr Ser Pro Gln Thr Val Pro Arg Leu Ile Asp Glu Ile Val Ile
850 855 860

Asn Pro His Tyr Asn Arg Arg Arg Lys Asp Asn Asp Ile Ala Met Met
865 870 875 880

His Leu Glu Phe Lys Val Asn Tyr Thr Asp Tyr Ile Gln Pro Ile Cys
885 890 895

Leu Pro Glu Glu Asn Gln Val Phe Pro Pro Gly Arg Asn Cys Ser Ile
900 905 910

Ala Gly Trp Gly Thr Val Val Tyr Gln Gly Thr Thr Ala Asn Ile Leu
915 920 925

Gln Glu Ala Asp Val Pro Leu Leu Ser Asn Glu Arg Cys Gln Gln Gln
930 935 940

Met Pro Glu Tyr Asn Ile Thr Glu Asn Met Ile Cys Ala Gly Tyr Glu
945 950 955 960

Glu Gly Gly Ile Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Met
965 970 975

Cys Gln Glu Asn Asn Arg Trp Phe Leu Ala Gly Val Thr Ser Phe Gly
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Tyr Lys Cys Ala Leu Pro Asn Arg Pro Gly Val Tyr Ala Arg Val Ser
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<210> 268

<211> 1186

<212> DNA

<213> Homo sapiens

<400> 268

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<210> 269

<211> 367

<212> PRT

<213> Homo sapiens

<400> 269

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Met Gly Thr Val Leu Ser Leu Ser Pro Ala Ser Ser Ala Lys Gly Arg
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Arg Pro Gly Gly Leu Pro Glu Glu Lys Lys Lys Ala Pro Pro Ala Gly
          20           25           30

```

```

Asp Glu Ala Leu Gly Gly Tyr Gly Ala Pro Pro Val Gly Lys Gly Gly
          35           40           45

```

```

Lys Gly Glu Ser Arg Leu Lys Arg Pro Ser Val Leu Ile Ser Ala Leu
          50           55           60

```

```

Thr Trp Lys Arg Leu Val Ala Ala Ser Ala Lys Lys Lys Lys Gly Ser
65           70           75           80

```

Lys Lys Val Thr Pro Lys Pro Ala Ser Thr Gly Pro Asp Pro Leu Val
 85 90 95

Gln Gln Arg Asn Arg Glu Asn Leu Leu Arg Lys Gly Arg Asp Pro Pro
 100 105 110

Asp Gly Gly Gly Thr Ala Lys Pro Leu Ala Val Pro Val Pro Thr Val
 115 120 125

Pro Ala Ala Ala Ala Thr Cys Glu Pro Pro Ser Gly Gly Ser Ala Ala
 130 135 140

Ala Gln Pro Pro Gly Ser Gly Gly Gly Lys Pro Pro Pro Pro Pro Pro
 145 150 155 160

Pro Ala Pro Gln Val Ala Pro Pro Val Pro Gly Gly Ser Pro Arg Arg
 165 170 175

Val Ile Val Gln Ala Ser Thr Gly Glu Leu Leu Arg Cys Leu Gly Asp
 180 185 190

Phe Val Cys Arg Arg Cys Tyr Arg Leu Lys Glu Leu Ser Pro Gly Glu
 195 200 205

Leu Val Gly Trp Phe Arg Gly Val Asp Arg Ser Leu Leu Leu Gln Gly
 210 215 220

Trp Gln Asp Gln Ala Phe Ile Thr Pro Ala Asn Leu Val Phe Val Tyr
 225 230 235 240

Leu Leu Cys Arg Glu Ser Leu Arg Gly Asp Glu Leu Ala Ser Ala Ala
 245 250 255

Glu Leu Gln Ala Ala Phe Leu Thr Cys Leu Tyr Leu Ala Tyr Ser Tyr
 260 265 270

Met Gly Asn Glu Ile Ser Tyr Pro Leu Lys Pro Phe Leu Val Glu Pro
 275 280 285

Asp Lys Glu Arg Phe Trp Gln Arg Cys Leu Arg Leu Ile Gln Arg Leu
 290 295 300

Ser Pro Gln Met Leu Arg Leu Asn Ala Asp Pro His Phe Phe Thr Gln
 305 310 315 320

Val Phe Gln Asp Leu Lys Asn Glu Gly Glu Ala Ala Ala Ser Gly Gly
 325 330 335

Gly Pro Pro Ser Gly Gly Ala Pro Ala Ala Ser Ser Ala Ala Arg Asp
 340 345 350

Ser Cys Ala Ala Gly Thr Lys His Trp Thr Met Asn Leu Asp Arg
 355 360 365

<210> 270
 <211> 513
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (457)..(457)
 <223> n = unknown

<220>
 <221> misc_feature
 <222> (497)..(497)
 <223> n = unknown

<220>
 <221> misc_feature
 <222> (499)..(499)
 <223> n = unknown

<220>
 <221> misc_feature
 <222> (509)..(509)
 <223> n = unknown

<400> 270
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 agcaaaatgt aacagatgct agattcccta aagtacggcg ctttaggtta catttgcaac 180
 aatagcttac atctaaatgt tacattagtt actgaatttg taatcttcac aaatgtgtga 240
 atagtcagtt gatcaaaaat aacgatttcc tgctacaaga gaacgcatag cagaaaaatgt 300

tcccaacaca aagataatgt ttgagatgat ggatatccca attacactga tttgataatt 360
 atacattgaa tacatgtatc acaacatcag atgtatccct gaaaatatgt acaactatat 420
 cagttttaaag atataaaaaa aattttctgt ccaaagntaa atatgtacaa ctacgatata 480
 tcagttttaa gatacanana atataattnt ctg 513

<210> 271
 <211> 34
 <212> PRT
 <213> Homo sapiens

<400> 271

Met Leu Asp Ser Leu Lys Tyr Gly Ala Leu Gly Tyr Ile Cys Asn Asn
 1 5 10 15

Ser Leu His Leu Asn Val Thr Leu Val Thr Glu Phe Val Ile Phe Thr
 20 25 30

Asn Val

<210> 272
 <211> 408
 <212> DNA
 <213> Homo sapiens

<400> 272
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 tgttccttcc atctgttcac ttttttggtg ttgttggtgt cggcatgatt tttactgaga 180
 aaaatgtaaa acatccttgg ctttttggg aagtttaaaa tcttcccaaa ttgagccctc 240
 taagaattgt tttcccatth actgttggcc cttcttcctt tctgccacct tcaataacac 300
 acgaagaaat cgagagggaa cttctagcag tcctgagacc ccttgagaaa ccagaaaaag 360
 gtgccataca cctcctttt tggggtcttt tgtcttcctc acggagcc 408

<210> 273
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 273

Met Leu Phe Leu Phe Gly Ser Cys Ser Tyr Pro Gly Asn Ser Phe Gln
 1 5 10 15

Ser Thr Glu Ile Leu Leu Lys Ser Asn Phe Met Phe Leu Pro Ser Val
 20 25 30

His Phe Phe Val Val Val Val Val Gly Met Ile Phe Thr Glu Lys Asn
 35 40 45

Val Lys His Pro Trp Pro Phe Trp Glu Val
 50 55

<210> 274

<211> 1646

<212> DNA

<213> Homo sapiens

<400> 274

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 cgctctgcgg ggtgagccgg actccccaac tccggacgat cagcccagga ctgagagccc 180
 cgaagtcccc aaccacaagt aagcggcccc agaaggacaa gtctaggtcg ccgtccagag 240
 cgccatggcc gcgcccggcc ttcgtttgtg ccacatcgcc ttccacgtgc ccgccgggca 300
 gccctagcc cggaacctgc agcgctctt cggttccag ccctggctt cgcgggaggt 360
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 cgcagggctt ggagagccgc tgtacggcct ggatccgcgt cagcccgctgc ccagcgccac 480
 aaacctgtgc ttcgacgtgg cggacgcgg cgctgcaacc cgggagctgg cagcgctggg 540
 ctgcagcgtg cctgtccctc ccgttcgcgt gcgggacgcg cagggtgccg ccacttacgc 600
 cgtggtcagc tcgctgccc gcacccctcag cctgaccttg ctggagcgcg ctggctaccg 660
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 ccgcgtggac cacctgacct tggcctgcac ccccggcagc tccccacac ttttgcgctg 780
 gttccacgac tgctggggt tttgccactt gccgctgagc ccaggtgagg atcccgagct 840
 gggcctcgaa atgacagcag ggtttgggct tgggggactg aggcttacag ccctgcaggc 900
 ccagccgggc agcattgtcc ccactcttgt tctggctgag tcccttcgg gggcgacgac 960
 acgacaggac caggtggagc agttcctggc ccggcacaag gggccaggcc tgcagcacgt 1020

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tgcagggcac gagcctcacc tgcttgctcg acaggggatc ctgctagatg gtgataaagg 1200
caagtttctg cttcaggtct tcaccaagtc cttttttact gaggacactt tcttcctgga 1260
gctgattcag aggcaggggg ccactggctt tggtcagggc aacatcagag ctctgtggca 1320
gtccgtacag gagcaatctg ccaggagcca ggaagcctaa ggatgcccag ggctgggtgc 1380
agccagctgt cctgcagctc tggggagacc agcacagAAC tgaggaacat ctgcaggagg 1440
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tgccagaagc tgtgtctctc attgggctcc aaagagggtgg gattttttta aactaaaaca 1560
tttcttatat acagtctata ataaatatgt aagatacaaa gaacaataaa agaattacac 1620
actaggaaaa aaaaaaaaaa aaaaaa 1646

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<210> 275
<211> 393
<212> PRT
<213> Homo sapiens
<400> 275

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Met Thr Thr Tyr Ser Asp Lys Gly Ala Lys Pro Glu Arg Gly Arg Phe
1          5          10          15

```

```

Leu His Phe His Ser Val Thr Phe Trp Val Gly Asn Ala Lys Gln Ala
          20          25          30

```

```

Ala Ser Phe Tyr Cys Ser Lys Met Gly Phe Glu Pro Leu Ala Tyr Arg
          35          40          45

```

```

Gly Leu Glu Thr Gly Ser Arg Glu Val Val Ser His Val Ile Lys Gln
          50          55          60

```

```

Gly Lys Ile Val Phe Val Leu Ser Ser Ala Leu Asn Pro Trp Asn Lys
65          70          75          80

```

```

Glu Met Gly Asp His Leu Val Lys His Gly Asp Gly Val Lys Asp Ile
          85          90          95

```

```

Ala Phe Glu Val Glu Asp Cys Asp Tyr Ile Val Gln Lys Ala Arg Glu
          100          105          110

```

Arg Gly Ala Lys Ile Met Arg Glu Pro Trp Val Glu Gln Asp Lys Phe
 115 120 125

Gly Lys Val Lys Phe Ala Val Leu Gln Thr Tyr Gly Asp Thr Thr His
 130 135 140

Thr Leu Val Glu Lys Met Asn Tyr Ile Gly Gln Phe Leu Pro Gly Tyr
 145 150 155 160

Glu Ala Pro Ala Phe Met Asp Pro Leu Leu Pro Lys Leu Pro Lys Cys
 165 170 175

Ser Leu Glu Met Ile Asp His Ile Val Gly Asn Gln Pro Asp Gln Glu
 180 185 190

Met Val Ser Ala Ser Glu Trp Tyr Leu Lys Asn Leu Gln Phe His Arg
 195 200 205

Phe Trp Ser Val Asp Asp Thr Gln Val His Thr Glu Tyr Ser Ser Leu
 210 215 220

Arg Ser Ile Val Val Ala Asn Tyr Glu Glu Ser Ile Lys Met Pro Ile
 225 230 235 240

Asn Glu Pro Ala Pro Gly Lys Lys Lys Ser Gln Ile Gln Glu Tyr Val
 245 250 255

Asp Tyr Asn Gly Gly Ala Gly Val Gln His Ile Ala Leu Lys Thr Glu
 260 265 270

Asp Ile Ile Thr Ala Ile Arg His Leu Arg Glu Arg Gly Leu Glu Phe
 275 280 285

Leu Ser Val Pro Ser Thr Tyr Tyr Lys Gln Leu Arg Glu Lys Leu Lys
 290 295 300

Thr Ala Lys Ile Lys Val Lys Glu Asn Ile Asp Ala Leu Glu Glu Leu
 305 310 315 320

Lys Ile Leu Val Asp Tyr Asp Glu Lys Gly Tyr Leu Leu Gln Ile Phe
 325 330 335

Thr Lys Pro Val Gln Asp Arg Pro Thr Leu Phe Leu Glu Val Ile Gln
340 345 350

Arg His Asn His Gln Gly Phe Gly Ala Gly Asn Phe Asn Ser Leu Phe
355 360 365

Lys Ala Phe Glu Glu Glu Gln Asn Leu Arg Gly Asn Leu Thr Asn Met
370 375 380

Glu Thr Asn Gly Val Val Pro Gly Met
385 390

<210> 276

<211> 1913

<212> DNA

<213> Homo sapiens

<400> 276

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gcacgaggca ggccgaagtc cgcagccccg gctcggcgcc cgctgcttgc acctcccgga      60
tggtgctgac tgctccctaa gcggcgggcg cggcgagtcg tgaggacgcg ccgcggaggc      120
tgttcggggg cgaggcttcc cgtcgccggc acttcctctt gcggcgcccc tgcgcgggccg      180
gcccggcagg cgggatgagc ggccgcggtc ccgggaacgg ccgcgcacat gcgccccggc      240
tgcttctgct ctttctggtt ccgctgctgt gggccccggc tgcggtccgg gccggcccag      300
atgaagacct tagccaccgg aacaaagaac cgccggcgcc ggcccagcag ctgcagccgc      360
agcctgtggc tgtgcagggc cccgagccgg ccgggtcga gaaaatattt acaccagcag      420
ctccagttca taccaataaa gaagatcctg ctacccaaac taatttgga tttatccatg      480
catttgctgc tgccatatca gttattattg tatctgaatt gggtgataag acatttttta      540
tagcagccat catggcaatg cgctataacc gcctgaccgt gctggctggg gcaatgcttg      600
ccttgggact aatgacatgc ttgtcagttt tgtttggcta tgccaccaca gtcacccca      660
gggtctatac atactatggt tcaactgtat tatttgccat ttttggcatt agaatgcttc      720
gggaaggctt aaagatgagc cctgatgagg gtcaagagga actggaagaa gttcaagctg      780
aattaaagaa gaaagatgaa gaatttcaac gaaccaaact tttaaattga ccgggagatg      840
ttgaaacggg tacaagcata acagtacctc agaaaaagtg gttgcatttt atttcaccca      900
ttttgttca agctcttaca ttaacattct tagcagaatg gggatgatgc tctcaactaa      960
ctacaattgt attggcagct agagaggacc cctatggtgt agccgtgggt ggaactgtgg     1020

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ggcactgcct gtgcacggga ttggcagtaa ttggaggaag aatgatagca cagaaaatct 1080
ctgtcagaac tgtgacaatc ataggaggca tcgttttttt ggcgtttgca ttttctgcac 1140
tatttataag ccctgattct ggtttttaac gctgtttgtt catctatatt tagtttaaaa 1200
taggtagtat tatctttctg tacatagtgt acattacaac taaaagtgat gggaaaaata 1260
ctgtattttg taggcactgg attttgtgag tttgaccctt tattatgtct ggaggatata 1320
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tgtggggggt ttttcttctc ttcccaacct taattatggt ttaataggt cctcattttt 1440
cttttggtgc agaaccgttg tgcagtgggg tctaccatgc aattttcttt cagcactgac 1500
ccctttttaa ggaatacaaa ttttctcctt catcacttag gtgttttaag atgtttacct 1560
taaagttttc ttgggggaaag aatgaattaa tttctatttc ttaaaacatt tccctgagcc 1620
agtaaacagt agtttaatca ttgggtcttt caaaactagg tgtttaaaaa aagagacata 1680
tatgatattg ctgttatatc aataacatgg cacaacaaga actgtctgcc aggtcattct 1740
tcctcttttt tttttaattg ggtaggacac cccatataaa aaccatccat atttggccat 1800
gtgggattac ccaaataaaa gaggaatcca tggatggatt cagaattttt ttaaatttaa 1860
taaaccaacc aacccttggg tcccatattt aattaaaagg agggttgccc agt 1913

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<210> 277
 <211> 324
 <212> PRT
 <213> Homo sapiens

<400> 277

Met Ser Gly Arg Gly Ser Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu
 1 5 10 15

Leu Leu Leu Phe Leu Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg
 20 25 30

Ala Gly Pro Asp Glu Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala
 35 40 45

Pro Ala Gln Gln Leu Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu
 50 55 60

Pro Ala Arg Val Glu Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr
 65 70 75 80

Asn Lys Glu Asp Pro Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala
 85 90 95

Phe Val Ala Ala Ile Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys
 100 105 110

Thr Phe Phe Ile Ala Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr
 115 120 125

Val Leu Ala Gly Ala Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser
 130 135 140

Val Leu Phe Gly Tyr Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr
 145 150 155 160

Tyr Val Ser Thr Val Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg
 165 170 175

Glu Gly Leu Lys Met Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu
 180 185 190

Val Gln Ala Glu Leu Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys
 195 200 205

Leu Leu Asn Gly Pro Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val
 210 215 220

Pro Gln Lys Lys Trp Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala
 225 230 235 240

Leu Thr Leu Thr Phe Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr
 245 250 255

Thr Ile Val Leu Ala Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly
 260 265 270

Gly Thr Val Gly His Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly
 275 280 285

Arg Met Ile Ala Gln Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly
 290 295 300

Gly Ile Val Phe Leu Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro
 305 310 315 320

Asp Ser Gly Phe

<210> 278
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 278
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 ggaaacgaaa gcgtgccgca taagcctacc gtctaccgcc cgcacatcag gaacctcacg 120
 gtacttcagg gaagcagtta agtcaagccg gcgcgtcaca ggcaactcggc gtgcaagccg 180
 ccccgaggt gctaccgtct cttacctctc tctactttta ggaaacacgt tgtatccccg 240
 gaggggggtgc accgttcctg gaggtactgc aataccaggt cgatgcgtgg agtggacgga 300
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 aggacgtat 369

<210> 279
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 279

Ile Leu Leu Thr Ser Pro Lys Glu Glu Val Val Ala Phe Pro Lys Arg
 1 5 10 15

Ser Ser His Gly Gly Asn Glu Ser Val Pro His Lys Pro Thr Val Tyr
 20 25 30

Arg Pro His Ile Arg Asn Leu Thr Val Leu Gln Gly Ser Ser
 35 40 45

<210> 280
 <211> 1601
 <212> DNA
 <213> Homo sapiens

<400> 280
 agaggcggtg cggcacagag gagcgctcgc ttcacaaggt gaccctagct cccaccgcca 60

ccgccgcggt cgcgctccag acgccctcca gcagctccgc gccctcccag gcacccggcc	120
tttctttctc cctcttgcaa ccaagatccg tccggccgct ggagaccag ggagccggg	180
ttaggaactc acttggggct tccccctccc ccaccggaga gccccgggat ggagagccga	240
aaggacatgg ttgtgtttct ggatgggggt cagcttggca ctctggttgg caagagagtc	300
tcaaatttgt ccgaagccgt gggcagcccg ctgccggagc cgcccagaa aatggtgccc	360
cgtggttgcc tgagccctcg ggccgtccct ccggccaccc gggagcgcg cgggggaggc	420
ccggaggagg agccggtaga tggactcgca ggcagcgcg cggggcccgg cgccgagccc	480
caggtagctg gggcgccat gctcggcca ggacccccg cccctcagt cgacagctc	540
tccggacagg ggcaaccag tagctcggac accgagtcgg atttctatga agaaatcgag	600
gtgagctgca ccccggaact cgccaccggg aacgccgagt accagcacag caaagggctc	660
ggctccgagg cgctggtcgg cagtccgaac ggaggagcg agaccccaa gagcaacggc	720
ggcagtggtg ggggcggctc gcaaggcacc ctggcgtgca gcgccagtga ccagatgcgt	780
cgttaccgca ccgccttcac ccgagagcag attgcgcggc tggagaagga attctaccgg	840
gagaactacg tatccaggcc gcggagatgt gagctggcg ccgccctaaa cctgccgaa	900
accaccatca aggtgtggtt ccagaaccgg cgcagtgaagg acaagcggca gcgcctggcc	960
atgacgtggc cgcacccggc ggaccccgcc ttctacactt acatgatgag ccatgcgggc	1020
gccgcgggcg gcctgcccta ccccttcca tcgcacctgc ccctgcccta ctactcgccg	1080
gtgggcctgg gcgcgcgcat cgccgcctcc gccgcgcct cgcccttcag cggtcgtg	1140
cgcccgctcg acacgttccg cgtgctgtcg cagccctacc cgcgcccga actgctgtgc	1200
gccttccgcc acccgccgct ctaccccggg ccgcgcacg gactgggcg ctctgccggc	1260
ggccctgct cctgcctcgc ctgtcacagc ggcccgcca acgggtggc gcccgggct	1320
gccgcgcct cggaattcac ctgtgcctcc acctccgct cggactcct cctcacctc	1380
gcgccctcgg tgctcagcaa ggcctcctcc gtcgcgctgg accagagga ggaggtgccc	1440
ctcactagat aaggggcccg gctggtggct gccggtcca tgacgcccg ggggtcacc	1500
cccggcccgg gactcagcca gcctcgctc ctgcctcctc gctcctcgcc cctaggacgc	1560
caagggggaa aggagaggc ggaaaaggac cagcgggatc c	1601

<210> 281
 <211> 407
 <212> PRT

<213> Homo sapiens

<400> 281

Met Glu Ser Arg Lys Asp Met Val Val Phe Leu Asp Gly Gly Gln Leu
1 5 10 15

Gly Thr Leu Val Gly Lys Arg Val Ser Asn Leu Ser Glu Ala Val Gly
20 25 30

Ser Pro Leu Pro Glu Pro Pro Glu Lys Met Val Pro Arg Gly Cys Leu
35 40 45

Ser Pro Arg Ala Val Pro Pro Ala Thr Arg Glu Arg Gly Gly Gly Gly
50 55 60

Pro Glu Glu Glu Pro Val Asp Gly Leu Ala Gly Ser Ala Ala Gly Pro
65 70 75 80

Gly Ala Glu Pro Gln Val Ala Gly Ala Ala Met Leu Gly Pro Gly Pro
85 90 95

Pro Ala Pro Ser Val Asp Ser Leu Ser Gly Gln Gly Gln Pro Ser Ser
100 105 110

Ser Asp Thr Glu Ser Asp Phe Tyr Glu Glu Ile Glu Val Ser Cys Thr
115 120 125

Pro Asp Cys Ala Thr Gly Asn Ala Glu Tyr Gln His Ser Lys Gly Ser
130 135 140

Gly Ser Glu Ala Leu Val Gly Ser Pro Asn Gly Gly Ser Glu Thr Pro
145 150 155 160

Lys Ser Asn Gly Gly Ser Gly Gly Gly Gly Ser Gln Gly Thr Leu Ala
165 170 175

Cys Ser Ala Ser Asp Gln Met Arg Arg Tyr Arg Thr Ala Phe Thr Arg
180 185 190

Glu Gln Ile Ala Arg Leu Glu Lys Glu Phe Tyr Arg Glu Asn Tyr Val
195 200 205

Ser Arg Pro Arg Arg Cys Glu Leu Ala Ala Ala Leu Asn Leu Pro Glu
 210 215 220
 Thr Thr Ile Lys Val Trp Phe Gln Asn Arg Arg Met Lys Asp Lys Arg
 225 230 235 240
 Gln Arg Leu Ala Met Thr Trp Pro His Pro Ala Asp Pro Ala Phe Tyr
 245 250 255
 Thr Tyr Met Met Ser His Ala Ala Ala Ala Gly Gly Leu Pro Tyr Pro
 260 265 270
 Phe Pro Ser His Leu Pro Leu Pro Tyr Tyr Ser Pro Val Gly Leu Gly
 275 280 285
 Ala Ala Ser Ala Ala Ser Ala Ala Ala Ser Pro Phe Ser Gly Ser Leu
 290 295 300
 Arg Pro Leu Asp Thr Phe Arg Val Leu Ser Gln Pro Tyr Pro Arg Pro
 305 310 315 320
 Glu Leu Leu Cys Ala Phe Arg His Pro Pro Leu Tyr Pro Gly Pro Ala
 325 330 335
 His Gly Leu Gly Ala Ser Ala Gly Gly Pro Cys Ser Cys Leu Ala Cys
 340 345 350
 His Ser Gly Pro Ala Asn Gly Leu Ala Pro Arg Ala Ala Ala Ala Ser
 355 360 365
 Asp Phe Thr Cys Ala Ser Thr Ser Arg Ser Asp Ser Phe Leu Thr Phe
 370 375 380
 Ala Pro Ser Val Leu Ser Lys Ala Ser Ser Val Ala Leu Asp Gln Arg
 385 390 395 400
 Glu Glu Val Pro Leu Thr Arg
 405

<210> 282
 <211> 201
 <212> DNA
 <213> Homo sapiens

<400> 282
 atcatgatcg ctctacatcg atacgacttt ttcttttttt tttttttttt ttttgcctag 60
 tatgaaaata taccaatac caccctcttt attgctgact gggaatgtcc tctcaaagct 120
 cctaaaattc ttgactgtct ccttttttgc ctttctctag ctggactatt ttgattatac 180
 ccttctgtcg tcttctcgca g 201

<210> 283
 <211> 32
 <212> PRT
 <213> Homo sapiens

<400> 283

Met Lys Ile Tyr Pro Ile Pro Pro Ser Leu Leu Leu Thr Gly Asn Val
 1 5 10 15

Leu Ser Lys Leu Leu Lys Phe Leu Thr Val Ser Phe Phe Ala Phe Leu
 20 25 30

<210> 284
 <211> 661
 <212> DNA
 <213> Homo sapiens

<400> 284
 ggagtggcag ccggagtctg aactgtcctg ggggaccaag caggagctta agatgggcaa 60
 gacctggggc cctgggcaga cgcataaag caggcagaag caggcatggc cagcaggaag 120
 accaagaaga aggaaggggg tgccctccgg gccagagag cctcatocaa tgtcttctcc 180
 aactttgagc agactcagat ccaggagttc aaggaggcat tcacactcat ggatcagaac 240
 cgagatggct tcattgacaa ggaggacctg aaggacacct atgcctccct gggcaagacc 300
 aacgtcaagg acgacgagct ggacgccatg ctcaaagagg cctcggggcc catcaacttc 360
 accatgtttc tgaacctgtt tggggagaag ctgagcggtg ccgacgccga ggagaccatt 420
 cttaacgcct tcaagatgct ggacccggac gggaaaggga aaatcaacaa ggagtacatc 480
 aagcgtctgc tgatgtccca ggctgacaag atgacggcgg aagaggtgga ccagatgttc 540
 cagttcgcct ccatcgatgt ggcgggcaac ctggactaca aggcgctcag ctacgtgatc 600
 acccacgggg aggagaagga ggagtgaac ccagccgggt caataaacct ggacgcttgg 660
 a 661

<210> 285
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 285

Met Ala Ser Arg Lys Thr Lys Lys Lys Glu Gly Gly Ala Leu Arg Ala
 1 5 10 15

Gln Arg Ala Ser Ser Asn Val Phe Ser Asn Phe Glu Gln Thr Gln Ile
 20 25 30

Gln Glu Phe Lys Glu Ala Phe Thr Leu Met Asp Gln Asn Arg Asp Gly
 35 40 45

Phe Ile Asp Lys Glu Asp Leu Lys Asp Thr Tyr Ala Ser Leu Gly Lys
 50 55 60

Thr Asn Val Lys Asp Asp Glu Leu Asp Ala Met Leu Lys Glu Ala Ser
 65 70 75 80

Gly Pro Ile Asn Phe Thr Met Phe Leu Asn Leu Phe Gly Glu Lys Leu
 85 90 95

Ser Gly Thr Asp Ala Glu Glu Thr Ile Leu Asn Ala Phe Lys Met Leu
 100 105 110

Asp Pro Asp Gly Lys Gly Lys Ile Asn Lys Glu Tyr Ile Lys Arg Leu
 115 120 125

Leu Met Ser Gln Ala Asp Lys Met Thr Ala Glu Glu Val Asp Gln Met
 130 135 140

Phe Gln Phe Ala Ser Ile Asp Val Ala Gly Asn Leu Asp Tyr Lys Ala
 145 150 155 160

Leu Ser Tyr Val Ile Thr His Gly Glu Glu Lys Glu Glu
 165 170

<210> 286
 <211> 296
 <212> DNA
 <213> Homo sapiens

<400> 286
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 gtaaacattg ccggatacat ttccatacgt ttttaaagaa tagaggagga ggaagaggag 120
 ggaaaaaaag gaaaataaat aaataaacgt gtggagcaat caactccaga atcacaccaa 180
 tattttctagg tctaattggcc acacagcaaa atcagcctca gttatcccat tgtcttcata 240
 tcttaagacc ccgcgatcct ggccttctcg taagctcccc ggacccgggc gtcctc 296

<210> 287
 <211> 34
 <212> PRT
 <213> Homo sapiens

<400> 287

Met Ala Thr Gln Gln Asn Gln Pro Gln Leu Ser His Cys Leu His Ile
 1 5 10 15

Leu Arg Pro Arg Asp Pro Gly Leu Leu Val Ser Ser Pro Asp Pro Gly
 20 25 30

Val Leu

<210> 288
 <211> 2076
 <212> DNA
 <213> Homo sapiens

<400> 288
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 gtgggagtg agtcagcacc aagccaggct ccccgcgctt gccttgccct cacctgctcc 120
 tgctctctgc cagaggcagc atgggtccgca gggcaccatg gggcccgaca gagtgcagc 180
 acgagaactg tgcgagaacg acgacctggc caccagcctc gtcctggacc cctacctcgg 240
 tttccgcacc cataagatga acgtcaggct tatcgctacc tccgtgcctt cctgccggaa 300
 agtggcttta ccattcctgcc ctgcacgcgc tactccatgg agaccaacgg ggccaagatc 360
 gtgtccactc gtgcttgga aaagaatgag aagctggagc tgctgggtgg ctgcattgca 420
 gagctgcggg aggcagatga ggggctgctg agggccggtg agaatgactt cagcatcatg 480
 tactcaacct gcaagcggag tgctcagctg tggctggggc cagccgcctt catcaaccat 540
 gactgcaaac ccaactgcaa gtttgtgcct gcagatggga acgcagcctg cgtgaagggtg 600

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ctccgggaca ttgagcctgg ggacgaggtg acatgcttct acggcgaggg cttcttcggc 660
gagaagaatg agcactgtga atgccacacc tgtgagagga aaggtgaagg agctttccga 720
accaggccta gggagcccgc gttgccacca cggcccctgg acaagtacca gctgcgtgag 780
accaagcggc ggctgcagca aggcctggac agtggcagcc gacagggcct gctgggcccct 840
cgggcctgcg tgcacccatc cccgctgcgc cgggacccat tctgcgcgcg ctgccagccc 900
ctgcgcctgc cagcctgcag cgcccgccca gacacctcac ccctctggct ccagtggctg 960
cctcagcccc agccccgagt gcggccccgg aagcgccgac gccccggcc cggaggggcc 1020
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ccccactgcc gcctgcgagg agaggccctg gtggccctgg gccagcccc ccacgcccgc 1140
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gtggaccttc gtcgcctggc cccagcccca ccagctacc cagcccctgc tgggaccca 1260
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caggccggac ggggaggccc agcagggaga gagggtctct ctctagctg ctaccagga 1440
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caccctgcc ccagcctcag gactgcagga gccatccgcc cccctcagcc ccttctccc 1680
cagggagcaa agccataagg ggcaggggccc accccacggc atctcccag aagtacaggc 1740
ctcaggagga ggtggaactg atgtaggggg tggcactccc cagagactgc cctcacgagg 1800
ggactggggt cgctctcagc tctgcagctg tctgcgggtg ggggaagggt ggggggtgtc 1860
tggaggcatg ttcccctcac cccccccgt gggctctcagg gaggccgggt gtgacctcat 1920
ctttctcatg gtgctatcct ggtgctattg ggggtgggag ctccctcccc tccccacac 1980
cagaaagggg tatgttgggg gcttgggaagc acttgaactt tttattttat taaaacctg 2040
ttataagcag caaaaaaaaa aaaaaaaaaa aaaaaa 2076

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<210> 289
<211> 346
<212> PRT
<213> Homo sapiens

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<400> 289

Met Glu Thr Asn Gly Ala Lys Ile Val Ser Thr Arg Ala Trp Lys Lys
1 5 10 15

Asn Glu Lys Leu Glu Leu Leu Val Gly Cys Ile Ala Glu Leu Arg Glu
20 25 30

Ala Asp Glu Gly Leu Leu Arg Ala Gly Glu Asn Asp Phe Ser Ile Met
35 40 45

Tyr Ser Thr Arg Lys Arg Ser Ala Gln Leu Trp Leu Gly Pro Ala Ala
50 55 60

Phe Ile Asn His Asp Cys Lys Pro Asn Cys Lys Phe Val Pro Ala Asp
65 70 75 80

Gly Asn Ala Ala Cys Val Lys Val Leu Arg Asp Ile Glu Pro Gly Asp
85 90 95

Glu Val Thr Cys Phe Tyr Gly Glu Gly Phe Phe Gly Glu Lys Asn Glu
100 105 110

His Cys Glu Cys His Thr Cys Glu Arg Lys Gly Glu Gly Ala Phe Arg
115 120 125

Thr Arg Pro Arg Glu Pro Ala Leu Pro Pro Arg Pro Leu Asp Lys Tyr
130 135 140

Gln Leu Arg Glu Thr Lys Arg Arg Leu Gln Gln Gly Leu Asp Ser Gly
145 150 155 160

Ser Arg Gln Gly Leu Leu Gly Pro Arg Ala Cys Val His Pro Ser Pro
165 170 175

Leu Arg Arg Asp Pro Phe Cys Ala Ala Cys Gln Pro Leu Arg Leu Pro
180 185 190

Ala Cys Ser Ala Arg Pro Asp Thr Ser Pro Leu Trp Leu Gln Trp Leu
195 200 205

Pro Gln Pro Gln Pro Arg Val Arg Pro Arg Lys Arg Arg Arg Pro Arg
210 215 220

Pro Arg Arg Ala Pro Val Leu Ser Thr His His Ala Ala Arg Val Ser
225 230 235 240

Leu His Arg Trp Gly Gly Cys Gly Pro His Cys Arg Leu Arg Gly Glu
245 250 255

Ala Leu Val Ala Leu Gly Gln Pro Pro His Ala Arg Trp Ala Pro Gln
260 265 270

Gln Asp Trp His Trp Ala Arg Arg Tyr Gly Leu Pro Tyr Val Val Arg
275 280 285

Val Asp Leu Arg Arg Leu Ala Pro Ala Pro Pro Ala Thr Pro Ala Pro
290 295 300

Ala Gly Thr Pro Gly Pro Ile Leu Ile Pro Lys Gln Ala Leu Ala Phe
305 310 315 320

Ala Pro Phe Ser Pro Pro Lys Arg Leu Arg Leu Val Val Ser His Ser
325 330 335

Ile Asp Leu Asp Val Gly Gly Glu Glu Leu
340 345

<210> 290
<211> 377
<212> DNA
<213> Homo sapiens

<400> 290
ctactactac tactaaattc gcggccgcgt cgactttttt tttttttttt agagatgggg 60
tctcgctcag tcaccaggc tagagtgcaa tgacacgaca tagctcactg tagcctcgga 120
ctcctgggct caagcaatcc tcccacctca gcctctggag tagctgggac cacaggtgca 180
agctactatg cctgtctcta ttatacctta catacatttt cacagttgtc tatttcctta 240
ttatcatttg tctcttctta ctgtgttcac tgtaccact tgttttaaat atattttattc 300
ctcgccttat tccaaagtct ttatcggttt tatagattgc atttaaaatc tgatattttg 360
acgtcgacgc ggccgcg 377

<210> 291
<211> 673

<212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(673)
 <223> X = unknown

<400> 291

Gly Trp Val Trp Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Glu Thr
 1 5 10 15

Arg Arg Ala Asp His Leu Arg Ser Gly Val Xaa Asp Gln Pro Asp Gln
 20 25 30

His Gly Glu Thr Val Ser Leu Leu Lys Ile His Lys Leu Ala Arg Asn
 35 40 45

Gly Gly Pro Cys Leu Xaa Ser Gln Leu His Gly Arg Gln Arg Gln Glu
 50 55 60

Asn Arg Leu Asn Pro Gly Gly Xaa Gly Cys Ser Glu Pro Lys Leu Ala
 65 70 75 80

Thr Ala Leu Gln Pro Gly Cys Gln Ser Lys Gly Leu Ser Gln Lys Gln
 85 90 95

Lys Gln Ser Lys Lys Lys Lys Lys Lys Thr Pro Lys Asn Lys Xaa Xaa
 100 105 110

Xaa Ala Gly Cys Gly Gly Ser Arg Leu Ser Ser Gln His Phe Gly Arg
 115 120 125

Pro Gly Gly Gln Ile Thr Xaa Gly Gln Glu Phe Glu Thr Ser Leu Ile
 130 135 140

Asn Met Val Lys Leu Cys Leu Tyr Xaa Lys Tyr Ile Asn Xaa Pro Gly
 145 150 155 160

Met Ala Ala His Ala Cys Asn Pro Ser Tyr Thr Gly Asp Arg Gly Arg
 165 170 175

Arg Ile Ala Xaa Thr Gln Glu Val Glu Ala Ala Val Ser Gln Asn Leu

180	185	190
Pro Leu His Ser Ser Arg Gly Val Arg Ala Arg Ala Tyr Leu Lys Asn		
195	200	205
Lys Asn Lys Ala Lys Lys Lys Lys Lys Lys Pro Pro Lys Thr Lys Xaa		
210	215	220
Xaa Xaa Leu Gly Val Val Ala His Ala Cys His Pro Ser Thr Leu Gly		
225	230	240
Asp Gln Glu Gly Arg Ser Leu Glu Val Arg Ser Leu Arg Pro Ala Xaa		
245	250	255
Ser Thr Trp Xaa Asn Cys Val Ser Ile Lys Asn Thr Xaa Ile Ser Gln		
260	265	270
Glu Trp Arg Pro Met Pro Val Ile Pro Ala Thr Arg Glu Thr Glu Ala		
275	280	285
Gly Glu Ser Leu Glu Pro Arg Arg Leu Arg Leu Gln Xaa Ala Lys Thr		
290	295	300
Cys His Cys Thr Pro Ala Gly Val Ser Glu Gln Gly Pro Ile Ser Lys		
305	310	315
Thr Lys Thr Lys Gln Lys Lys Lys Lys Lys Asn Pro Gln Lys Gln Xaa		
325	330	335
Xaa Xaa Phe Cys Phe Trp Gly Phe Phe Phe Phe Phe Phe Cys Phe Val		
340	345	350
Phe Val Phe Glu Ile Gly Pro Cys Ser Asp Thr Pro Ala Gly Val Gln		
355	360	365
Trp Gln Val Leu Ala His Cys Ser Leu Asn Leu Leu Gly Ser Ser Asp		
370	375	380
Ser Pro Ala Ser Val Ser Arg Val Ala Gly Ile Thr Gly Met Gly Arg		
385	390	395
His Ser Trp Leu Ile Tyr Val Phe Leu Ile Glu Thr Gln Phe His His		

405 410 415
 Val Asp Gln Ala Gly Leu Lys Leu Leu Thr Ser Ser Asp Leu Pro Ser
 420 425 430
 Trp Ser Pro Lys Val Leu Gly Xaa Gln Ala Xaa Ala Thr Thr Pro Ser
 435 440 445
 Xaa Xaa Xaa Phe Val Phe Gly Gly Phe Phe Phe Phe Phe Phe Ala Leu
 450 455 460
 Phe Leu Phe Leu Arg Xaa Ala Leu Ala Leu Thr Pro Arg Leu Glu Cys
 465 470 475 480
 Ser Gly Lys Phe Trp Leu Thr Ala Ala Ser Thr Ser Trp Val Gln Ala
 485 490 495
 Ile Leu Leu Pro Leu Ser Pro Val Xaa Leu Gly Leu Gln Ala Trp Ala
 500 505 510
 Ala Ile Pro Gly Xaa Phe Met Tyr Phe Xaa Xaa Arg His Ser Phe Thr
 515 520 525
 Met Leu Ile Arg Leu Val Ser Asn Ser Xaa Pro Gln Val Ile Cys Pro
 530 535 540
 Pro Gly Leu Pro Lys Cys Trp Asp Asp Arg Arg Glu Pro Pro His Pro
 545 550 555 560
 Ala Xaa Xaa Xaa Leu Phe Leu Gly Val Phe Phe Phe Phe Phe Leu Leu
 565 570 575
 Cys Phe Cys Phe Xaa Asp Arg Pro Leu Leu Xaa His Pro Gly Trp Ser
 580 585 590
 Ala Val Ala Ser Phe Gly Ser Leu Gln Pro Gln Pro Pro Gly Phe Lys
 595 600 605
 Arg Phe Ser Cys Leu Cys Leu Pro Cys Ser Trp Asp Tyr Arg His Gly
 610 615 620
 Pro Pro Phe Leu Ala Asn Leu Cys Ile Phe Asn Arg Asp Thr Val Ser

625					630						635					640
Pro	Cys	Xaa	Ser	Gly	Trp	Ser	Gln	Thr	Pro	Asp	Leu	Lys	Xaa	Ser	Ala	
				645					650					655		
Leu	Leu	Val	Ser	Gln	Ser	Ala	Gly	Met	Thr	Gly	Val	Ser	His	His	Thr	
			660					665					670			

Gln

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<210> 292
<211> 125
<212> DNA
<213> Homo sapiens

<400> 292
gcggccgcgct actactacta tacggtcgcg agaagacgac agaagggcga aaaactcact      60
ctacctcctt gaaggggagtg caaggaaagt tgtcttgatg ccaggtaaaa caaaaaaaaaa      120
aaaaa                                           125
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<210> 293
<211> 33
<212> PRT
<213> Homo sapiens
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<400> 293

Leu Arg Glu Asp Asp Arg Arg Ala Lys Asn Ser Leu Tyr Leu Leu Glu
1 5 10 15
Gly Ser Ala Arg Lys Val Val Leu Met Pro Gly Lys Thr Lys Lys Lys
20 25 30

Lys

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<210> 294
<211> 854
<212> DNA
<213> Homo sapiens.

<400> 294
cccgatccc tgcggctgcc tgcactctgg accacgagct ctgagagcag caggttgagg      60
gccggtgggc agcagctcgg aggctccgcg aggtgcagga gacgcaggca tggccggtga      120

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gctgactcct gaggaggagg ccaggtacaa aaaggctttc tccgcggttg acacggatgg 180
 aaacggcacc atcaatgcc aggagctggg cgcggcgctg aaggccacgg gcaagaacct 240
 ctcgagggcc cagctaagga aactcatctc cgaggttgac agcgacggcg acggcgaaat 300
 cagcttcag gagttcctga cggcggaag gaaggccagg gccggcctgg aggacctgca 360
 ggtcgccttc cgcgccttcg accaggatgg cgacggccac atcacgtgg acgagctcag 420
 gcgggccatg gcggggctgg ggcagccgt gccgcaggag gagctggacg ccagatccg 480
 cgaggccgac gtggaccagg acgggcgggt gaactacgag gagttcgca ggatgctcgc 540
 ccaggagtga ggctccccgc ctgtgtcccc ctggctgcgc tctgagcctt cagggccacc 600
 gcccgctgct gcttttgtgc tgggactctc cggggaaacc tggtcggtgg atgggaaact 660
 gcctccccct gggaggaagg ctttgcgctc cggggcctgg atgcggcgcc ctcgggcgc 720
 ctgcgagccc ctctctgcct tcagaccttg ggcagaagga ggcctccttg ggcctggtcc 780
 ccctttgcc tgagtgga tgagggcccc ttaacccgc attgatctaa ataaaggact 840
 gccgagttcc aaaa 854

<210> 295
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 295

Met Ala Gly Glu Leu Thr Pro Glu Glu Glu Ala Gln Tyr Lys Lys Ala
1 5 10 15

Phe Ser Ala Val Asp Thr Asp Gly Asn Gly Thr Ile Asn Ala Gln Glu
20 25 30

Leu Gly Ala Ala Leu Lys Ala Thr Gly Lys Asn Leu Ser Glu Ala Gln
35 40 45

Leu Arg Lys Leu Ile Ser Glu Val Asp Ser Asp Gly Asp Gly Glu Ile
50 55 60

Ser Phe Gln Glu Phe Leu Thr Ala Ala Arg Lys Ala Arg Ala Gly Leu
65 70 75 80

Glu Asp Leu Gln Val Ala Phe Arg Ala Phe Asp Gln Asp Gly Asp Gly
85 90 95

His Ile Thr Val Asp Glu Leu Arg Arg Ala Met Ala Gly Leu Gly Gln
 100 105 110

Pro Leu Pro Gln Glu Glu Leu Asp Ala Met Ile Arg Glu Ala Asp Val
 115 120 125

Asp Gln Asp Gly Arg Val Asn Tyr Glu Glu Phe Ala Arg Met Leu Ala
 130 135 140

Gln Glu
 145

<210> 296
 <211> 154
 <212> DNA
 <213> Homo sapiens

<400> 296
 cgagaagacg acagaagggc aacatttgag ctgattctta aaaaaaaaaa aaaaaaaata 60
 gagatacacg agaaatccaa attaggatag aattccagaa gaaggagta gcatgtgcaa 120
 aaaaaaaaaa aaaaaaaaaa aaaagtcgta tcga 154

<210> 297
 <211> 29
 <212> PRT
 <213> Homo sapiens

<400> 297

Arg Glu Asp Asp Arg Arg Ala Thr Phe Glu Leu Ile Leu Lys Lys Lys
 1 5 10 15

Lys Lys Lys Ile Glu Ile His Glu Lys Ser Lys Leu Gly
 20 25

<210> 298
 <211> 452
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(452)
 <223> n = unknown

<400> 298
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 gccagctag tttcttttat ttttggtaga gtcagggttt cgccttggtg cccagatag 180
 tcttgaactc ctgagttcta gccatccacc cgcctctggc cctcaaagt gctgggatta 240
 taggcgtcac ccaccacgcc cagccagagt aagccttttg tgtgtttatc anaticanccc 300
 ccnctncnna atatgttata ctgttgcgag tgacagaaga ggaaacagcc acagaaaggt 360
 aattgctcaa ggctgcagag ttaagtgcta gagctggatt caaatccagg cagtccagct 420
 acagaacact gctgctgtgc gctcgggatg gg 452

<210> 299
 <211> 375
 <212> PRT
 <213> Homo sapiens

<400> 299

Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile
 1 5 10 15

Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala
 20 25 30

Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
 35 40 45

Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
 50 55 60

Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
 65 70 75 80

Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu
 85 90 95

Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
 100 105 110

Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
 115 120 125

Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
 130 135 140
 Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp
 145 150 155 160
 His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
 165 170 175
 Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
 180 185 190
 Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
 195 200 205
 Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
 210 215 220
 Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
 225 230 235 240
 Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
 245 250 255
 Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
 260 265 270
 Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
 275 280 285
 Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
 290 295 300
 Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
 305 310 315 320
 Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
 325 330 335
 Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
 340 345 350

Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp
 355 360 365

Ser Gln Thr Pro Asp Leu Arg
 370 375

<210> 300
 <211> 496
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (11)..(11)
 <223> n = unknown

<400> 300
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 aatccttatg actctgttta aaatgagtat ctgcattatt gtgcaaacac ttctgagatc 180
 tcatcacata cctgatccca tttaacttca gtctatccct ccattacttt ttgtggaaag 240
 tgctatctaa gttggagggt ctgcttgagt attcttaatt tttcttcttt ttaatgcata 300
 cggtggtcaa agtaaatagc taacatattg gcatcaaacc attgcctatt gaagcaagct 360
 ttgaatgaaa ttggtttgtc attgaccact gtgagaaact catttgtaaa gataatactg 420
 aaaaacatcc tgactcttat gtatgcttgc ctgtctctga actccacctc taccagcata 480
 ctcaatacat tgcctc 496

<210> 301
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 301

Leu Ala Ser Asn His Cys Leu Leu Lys Gln Ala Leu Asn Glu Ile Gly
 1 5 10 15

Leu Ser Leu Thr Thr Val Arg Asn Ser Phe Val Lys Ile Ile Leu Lys
 20 25 30

Asn Ile Leu Thr Leu Met Tyr Ala Cys Leu Ser Leu Asn Ser Thr Ser
 35 40 45

Ile Ser Ile Leu Asn Thr Leu Pro
50 55

<210> 302

<211> 456

<212> DNA

<213> Homo sapiens

<400> 302

tttaactctt agaatccaag tgactcatct gtgtgcttga atcctttcca ctgtctcatc 60
tccctcatcc aagtttctag taccttctct ttgttgtaga ggataatcaa actgaacaac 120
aaaaagttta ctctcctcat ttggaaccta aaaactctct tcttcctggg tctgagggct 180
ccaagaatcc ttgaatcagt tctcagatca ttgtggacac cagatcagga acctcaggca 240
cgtgggaaag gccagataat taggagggat gctgaagaga aagcccgatg accacagcac 300
ggatgatggt taaaggcctt gaaatttggg taccatcatt cccaaccca ccaaccgccc 360
atgggtagca ttcaccagca cgcactggca gccgcagcca cccgttctct ttccttgcat 420
tgctgagcaa gtttcccata tcattcagtt aggctc 456

<210> 303

<211> 43

<212> PRT

<213> Homo sapiens

<400> 303

Leu Val Thr Ile Ile Pro Gln Pro Thr Asn Arg Pro Trp Val Ala Phe
1 5 10 15

Thr Ser Thr His Trp Gln Pro Gln Pro Pro Val Leu Phe Pro Cys Ile
20 25 30

Ala Glu Gln Val Ser His Ile Ile Gln Leu Gly
35 40

<210> 304

<211> 354

<212> DNA

<213> Homo sapiens

<400> 304

tttctattga tgcaaacagg ctgttgcccta aagcaggggt taatactccc caccctagaa 60
agtgcacat cctcctccag ccctacttcc catgcaatgt ataagcatt gtacaaagga 120

acacacagggc acacacaaaac ttacacacat gcttttttct tggatgaaga ttcttacaca 180
 ccaacagtga gttcttcgaa aattacaatc taactgtata tcctggaata taagtggagc 240
 cacactacag accaaactga ggtccaggac ctgtactttt tgtacaatag aaccagctc 300
 ttctactggt ctgcagccag cagatggcag atctctgagc agaactgctt ttgg 354

<210> 305
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 305

Met Gln Thr Gly Cys Cys Leu Lys Gln Gly Leu Ile Leu Pro Thr Leu
 1 5 10 15

Glu Ser Asp Thr Ser Ser Ser Ser Pro Thr Ser His Ala Met Tyr Lys
 20 25 30

His Leu Tyr Lys Gly Thr His Arg His Thr Gln Thr Tyr Thr His Ala
 35 40 45

Phe Phe Leu Asp Glu Asp Ser Tyr Thr Pro Thr Val Ser Ser Ser Lys
 50 55 60

Ile Thr Ile
 65

<210> 306
 <211> 3892
 <212> DNA
 <213> Homo sapiens

<400> 306

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 aaaagcttca attaccatt gctctogtcc ccaggtgatc agcttgaaat tcagctaacc 120
 gacgagctac ggtccctcat cccaacgag gatgtgagaa agttcatgtc tcatgttata 180
 tggaccttga aaatggaatg ttcagaaaca catgtgcaag ggagctgtgc caagctcatg 240
 tcgcgaacag gcctcctgat gaagcttctc agcgagcagc aggaagcaaa ggcattgaat 300
 gtagaatggg atacggacca acaaaaaaca aattatatta atgagaacat ggaacagaat 360
 gaacagaaag agcagaagtc aagtgaagctc atgaaagaag ttccaggata tgactataag 420

aacaaactca tcttcgcaat atctgtgact gtcatactaa taattttgat tataatTTTT	480
tgttttatag aggtaaagac aataattaat tcaggttttc aaaatacaat cctgtgtttg	540
tgtggattca gaatccacaa actgaaaacc aacgtcactt tcccacttga cattcttctt	600
ctgtcattta aggctgaggt gtgctttggt cttttactgc aatgtatatt ccaggattgt	660
taaaggatcc tcgcttccag gaggtctctg tgaaataaaa ccaagttaat cccactagac	720
tattttaaga agttaagttg atataatagc aaaatttctc ccacccaaaa ctatgtcaac	780
aattggatgt actcactgag tcacccctta ctctgccact aatttatttc cttgttgctt	840
aaatgatgag agacatataa tctccaccct cacggagttg tcatcaccct ggagaggaag	900
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<210> 307

<211> 220

<212> PRT

<213> Homo sapiens

<400> 307

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Ser Pro Glu Pro Lys Ser Phe Asn Tyr Pro Leu Leu Ser Ser Pro Gly
20 25 30

Asp Gln Leu Glu Ile Gln Leu Thr Glu Gln Leu Arg Ser Leu Ile Pro
35 40 45

Asn Glu Asp Val Arg Lys Phe Met Ser His Val Ile Trp Thr Leu Lys
50 55 60

Met Glu Cys Ser Glu Thr His Val Gln Gly Ser Cys Ala Lys Leu Met
65 70 75 80

Ser Arg Thr Gly Leu Leu Met Lys Leu Leu Ser Glu Gln Gln Glu Ala
85 90 95

Lys Ala Leu Asn Val Glu Trp Asp Thr Asp Gln Gln Lys Thr Asn Tyr
100 105 110

Ile Asn Glu Asn Met Glu Gln Asn Glu Gln Lys Glu Gln Lys Ser Ser
115 120 125

Glu Leu Met Lys Glu Val Pro Gly Tyr Asp Tyr Lys Asn Lys Leu Ile
130 135 140

Phe Ala Ile Ser Val Thr Val Ile Leu Ile Ile Leu Ile Ile Ile Phe
145 150 155 160

Cys Phe Ile Glu Val Lys Thr Ile Ile Asn Ser Gly Phe Gln Asn Thr
165 170 175

Ile Leu Cys Leu Cys Gly Phe Arg Ile His Lys Leu Lys Thr Asn Val
 180 185 190

Thr Phe Pro Leu Asp Ile Leu Leu Leu Ser Phe Lys Ala Glu Val Cys
 195 200 205

Phe Val Leu Leu Leu Gln Cys Ile Phe Gln Asp Cys
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<210> 308

<211> 2492

<212> DNA

<213> Homo sapiens

<400> 308

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<210> 309

<211> 103

<212> PRT

<213> Homo sapiens

<400> 309

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20 25 30

Pro Pro Arg Pro Pro Lys Val Leu Gly Leu Ile Thr Gly Val Ser His
35 40 45

Tyr Ala Gln Pro Pro Trp Ser Tyr Phe Tyr Leu Lys His Ile His Tyr
50 55 60

Asn Ser Ile Asp Leu Ile Thr Lys Val Pro Ile Leu Leu Lys Cys Phe
65 70 75 80

Ile Val Ile Lys Ile Gln Lys Leu Leu Met Leu Ala Asn Lys Ile Gln
85 90 95

Ala Lys His Lys Cys Val Lys
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<210> 310
<211> 2985
<212> DNA
<213> Homo sapiens

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<210> 311
<211> 474
<212> PRT
<213> Homo sapiens

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<400> 311

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Glu Trp Lys Cys Leu Asp Pro Asp Gln Gln Asn Leu Tyr Arg Asp Val
20          25          30

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Met Leu Glu Asn Tyr Arg Asn Leu Val Ser Leu Gly Val Ala Ile Ser
35          40          45

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Asn Pro Asp Leu Val Thr Cys Leu Glu Gln Arg Lys Glu Pro Tyr Asn
50          55          60

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Val Lys Ile His Lys Ile Val Ala Arg Pro Pro Ala Met Cys Ser His
65          70          75          80

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Phe Thr Gln Asp His Trp Pro Val Gln Gly Ile Glu Asp Ser Phe His
85          90          95

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Lys Leu Ile Leu Arg Arg Tyr Glu Lys Cys Gly His Asp Asn Leu Gln
100         105         110

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Leu Arg Lys Gly Cys Lys Ser Leu Asn Glu Cys Lys Leu Gln Lys Gly
115         120         125

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Gly Tyr Asn Glu Phe Asn Glu Cys Leu Ser Thr Thr Gln Ser Lys Ile
 130 135 140

Leu Gln Cys Lys Ala Ser Val Lys Val Val Ser Lys Phe Ser Asn Ser
 145 150 155 160

Asn Lys Arg Lys Thr Arg His Thr Gly Glu Lys His Phe Lys Glu Cys
 165 170 175

Gly Lys Ser Phe Gln Lys Phe Ser His Leu Thr Gln His Lys Val Ile
 180 185 190

His Ala Gly Glu Lys Pro Tyr Thr Cys Glu Glu Cys Gly Lys Ala Phe
 195 200 205

Lys Trp Ser Leu Ile Phe Asn Glu His Lys Arg Ile His Thr Gly Glu
 210 215 220

Lys Pro Phe Thr Cys Glu Glu Cys Gly Ser Ile Phe Thr Thr Ser Ser
 225 230 235 240

His Phe Ala Lys His Lys Ile Ile His Thr Gly Glu Lys Pro Tyr Lys
 245 250 255

Cys Glu Glu Cys Gly Lys Ala Phe Asn Arg Phe Thr Thr Leu Thr Lys
 260 265 270

His Lys Arg Ile His Ala Gly Glu Lys Pro Ile Thr Cys Glu Glu Cys
 275 280 285

Arg Lys Ile Phe Thr Ser Ser Ser Asn Phe Ala Lys His Lys Arg Ile
 290 295 300

His Thr Gly Glu Lys Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe
 305 310 315 320

Asn Arg Ser Thr Thr Leu Thr Lys His Lys Arg Ile His Thr Gly Glu
 325 330 335

Lys Pro Tyr Thr Cys Glu Glu Cys Gly Lys Ala Phe Arg Gln Ser Ser
 340 345 350

Lys Leu Asn Glu His Lys Lys Val His Thr Gly Glu Arg Pro Tyr Lys
355 360 365

Cys Asp Glu Cys Gly Lys Ala Phe Gly Arg Ser Arg Val Leu Asn Glu
370 375 380

His Lys Lys Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Glu Glu Cys
385 390 395 400

Gly Lys Ala Phe Arg Arg Ser Thr Asp Arg Ser Gln His Lys Lys Ile
405 410 415

His Ser Ala Asp Lys Pro Tyr Lys Cys Lys Glu Cys Asp Lys Ala Phe
420 425 430

Lys Gln Phe Ser Leu Leu Ser Gln His Lys Lys Ile His Thr Val Asp
435 440 445

Lys Pro Tyr Lys Cys Lys Asp Cys Asp Lys Ala Phe Lys Arg Phe Ser
450 455 460

His Leu Asn Lys His Lys Lys Ile His Thr
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<210> 312
<211> 540
<212> DNA
<213> Homo sapiens

<400> 312
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<210> 313
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 313

Met Leu Lys Gln Ser Lys Thr Phe Cys Asn Tyr Ser Ser Ala Cys Asn
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Thr Leu Pro Cys Phe Ile Ser Asp Cys Phe Thr Ser Lys Met Ser Phe
 20 25 30

Gln Cys His Leu Thr Gly Glu Ala Phe Leu Asp His Pro Ile
 35 40 45

<210> 314
 <211> 500
 <212> DNA
 <213> Homo sapiens

<400> 314

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<210> 315
 <211> 65
 <212> PRT
 <213> Homo sapiens

<400> 315

Met Pro Ser Trp Ala Ala Pro Ser Pro Ser Val Ser Cys Pro Asp Leu
 1 5 10 15

Ala Ser Pro His Leu Ser Val Thr Arg His Met Val Gln Ala Gly Leu

20

25

30

Gln Gln Asn Phe Pro Gln Leu Gln His Ser Gln Cys Leu Ala Leu Asp
 35 40 45

Phe Gln Phe His Leu Val Glu Leu Gly His Gly Thr Lys Asp Arg Asn
 50 55 60

Lys
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<210> 316

<211> 468

<212> DNA

<213> Homo sapiens

<400> 316

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tgctgtagt tggagggtta gagagaggga tcaataattt catggttg 468

<210> 317

<211> 49

<212> PRT

<213> Homo sapiens

<400> 317

Met Asp Trp Asp Arg Glu Gly Leu Leu Thr His Thr His Thr Glu Ala
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Ile Asn Leu Gly Ser Ser Arg Ser Arg Arg Leu Thr Ala Ser Arg Pro
 20 25 30

Val Ala Glu Cys Thr Pro Ala Leu Gly Asn Val Trp Ala Ala Ser Cys
 35 40 45

Leu

<210> 318
 <211> 490
 <212> DNA
 <213> Homo sapiens

<400> 318
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 cttgggtagc tgttcaatgt tatatatatg ggaaaacatg tgttgtgcac ttttctacat 300
 gtgtatattc ttcacaatat tttaaataaa taaagcaagc aactatgtat tagcagatag 360
 aaaaatgata aagtgataga tctaatacct ggttatttaa aataaataaa tagataaaact 420
 tctggctgat ttaaagcaga ataaaaagtg aaaaagtcaa ttacataaaa taggaaaata 480
 taatttacgg 490

<210> 319
 <211> 33
 <212> PRT
 <213> Homo sapiens

<400> 319

Met Arg Trp Thr Phe Asp Leu Gly Ser Cys Ser Met Leu Tyr Ile Trp
 1 5 10 15

Glu Asn Met Cys Cys Ala Leu Phe Tyr Met Cys Ile Phe Phe Thr Ile
 20 25 30

Phe

<210> 320
 <211> 449
 <212> DNA
 <213> Homo sapiens

<400> 320
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 cataaaaagcc ccagtaaagt ccacagaaaa cccagaaaaa acagcagcag tcacaaagac 180
 tataaaacct tcagtcaagg tcacaggaga caaatctctc actactacct cttctcatct 240
 aaataaaaact gaagttactc atcaggtgcc cactggttct ttcacctca ttacatctag 300
 aacgaagctg agttctatca catcagaagc cacaggaaac gagagccatc catacctcaa 360
 taaagatggc tcacagaaag gtatccacgc tggacagatg ggagagaatg attcattccc 420
 tgcatgggcc atagttattg tggctctgg 449

<210> 321
 <211> 235
 <212> PRT
 <213> Homo sapiens

<400> 321

Met Thr Gln Val Thr Glu Lys Ser Thr Glu His Pro Glu Lys Thr Thr
1 5 10 15

Ser Thr Thr Glu Lys Thr Thr Arg Thr Pro Glu Lys Pro Thr Leu Tyr
20 25 30

Ser Glu Lys Thr Ile Cys Thr Lys Gly Lys Asn Thr Pro Val Pro Glu
35 40 45

Lys Pro Thr Glu Asn Leu Gly Asn Thr Thr Leu Thr Thr Glu Thr Ile
50 55 60

Lys Ala Pro Val Lys Ser Thr Glu Asn Pro Glu Lys Thr Ala Ala Val
65 70 75 80

Thr Lys Thr Ile Lys Pro Ser Val Lys Val Thr Gly Asp Lys Ser Leu
85 90 95

Thr Thr Thr Ser Ser His Leu Asn Lys Thr Glu Val Thr His Gln Val
100 105 110

Pro Thr Gly Ser Phe Thr Leu Ile Thr Ser Arg Thr Lys Leu Ser Ser
115 120 125

Ile Thr Ser Glu Ala Thr Gly Asn Glu Ser His Pro Tyr Leu Asn Lys
130 135 140

Asp Gly Ser Gln Lys Gly Ile His Ala Gly Gln Met Gly Glu Asn Asp
145 150 155 160

Ser Phe Pro Ala Trp Ala Ile Val Ile Val Val Leu Val Ala Val Ile
165 170 175

Leu Leu Leu Val Phe Leu Gly Leu Ile Phe Leu Val Ser Tyr Met Met
180 185 190

Arg Thr Arg Arg Thr Leu Thr Gln Asn Thr Gln Tyr Asn Asp Ala Glu
195 200 205

Asp Glu Gly Gly Pro Asn Ser Tyr Pro Val Tyr Leu Met Glu Gln Gln
210 215 220

Asn Leu Gly Met Gly Gln Ile Pro Ser Pro Arg
225 230 235

<210> 322
<211> 419
<212> DNA
<213> Homo sapiens

<400> 322
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aagggtgtggg aaccgttttag tcacagacac cgtcccgtct acctcccccg agtccagcct 180
tgggtgggtg ctgcacagcg acttgcggcc ttaggtcttc tcgctgtgcc ttcctttcct 240
cctgagagat gctctccgcc taagaccgct aacagctcaa ttgggtctca ttgatccac 300
tcaccatcta gagccctgtt gcctcattaa tccgttgtgc caccagctca cgggctgcaa 360
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<210> 323
<211> 97
<212> PRT
<213> Homo sapiens

<400> 323

Phe Pro His Thr Pro Ser Pro Gln Thr Asn Ile Ser Gly Phe Thr Gly
1 5 10 15

Thr Cys Arg Leu Leu Gly Thr Gly Leu Asp Phe Ile Arg His Leu Ser
 20 25 30

Lys His Asn Pro Gly Ala Ala Cys Lys Val Trp Glu Pro Phe Ser His
 35 40 45

Arg His Arg Pro Val Tyr Leu Pro Arg Val Gln Pro Trp Val Gly Ala
 50 55 60

Ala Gln Arg Leu Ala Ala Leu Gly Leu Leu Ala Val Pro Ser Phe Pro
 65 70 75 80

Pro Glu Arg Cys Ser Pro Pro Lys Thr Ala Asn Ser Ser Ile Gly Ser
 85 90 95

His

<210> 324
 <211> 573
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc feature
 <222> (475)..(475)
 <223> n = unknown

<400> 324
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 tggggtttgg accatgccag gttttgctga ggaattgggg gatcggttac agaattatgg 180
 gaaggttggt tgactttcaa atcttcactt atcccctgcg atacatttgg cttcatgact 240
 gtttactgtg tggcttggtt gctagcgcac tctatctagg ttaagatatt gcttcctttc 300
 ttcaaattct tgccatgtgc tgattaattc ttctgttttt aatttttctt ttccctggat 360
 taattgccat ttcagagttt gcatgaaacc atataacact attgagaagt ttttggggaa 420
 ggctatcggg catttgagga ttttgcctac cataagcatg catcttttct accgngaato 480
 acgaggactc tactggactg agttcagtgg ctgagacaaa attacaatag ccaataacag 540
 taacagcagc agcagccaca gggttatcaag ctg 573

<210> 325
 <211> 43
 <212> PRT
 <213> Homo sapiens

<400> 325

Met Lys Pro Tyr Asn Thr Ile Glu Lys Phe Leu Gly Lys Ala Ile Gly
 1 5 10 15

His Leu Arg Ile Leu Pro Thr Ile Ser Met His Leu Phe Tyr Arg Glu
 20 25 30

Ser Arg Gly Leu Tyr Trp Thr Glu Phe Ser Gly
 35 40

<210> 326
 <211> 2351
 <212> DNA
 <213> Homo sapiens

<400> 326

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 gtttttaggga aattaacaaa aaaattocca gatgccaaaca gccaccattc aaaagaccac 180
 caatctattg catcatacca gatgccactc tctcttctta gtagggattt ctctcctcgg 240
 tcttgatcaa ggtgttataa tagagacatt ttcattatag acagtgtcct gaagggattc 300
 cagctcaaat ataggaattc ttaaacctag ctgaaactcc caaagtgatt tcattgctgg 360
 gcatatttta acatacttag gggaaagcaa atctttaaac aaagcaaac accaaactac 420
 agttttaaaa agaagaaagg agagcgtatt ttagtttcaa aattacatta cattttaatt 480
 taattttcct tctaattttc ctgtcagcat tttatttaca aaaactgtgc agcaaacgag 540
 ggaaaatctt ccaacacaaa caactctgta atgactaaat tggttttatt catatatattt 600
 agacatttgg ttaacttgga tctttttcat aagttctttg tgatgctttg taagggttagt 660
 gtaactgaag tgtttgtgag tttgatttgg tcccacagtg cttaattcag tggatatattt 720
 gctagaagtt ttaatgtaaa cttgggtggt taactgacta ttaagtgtaa cctattgtga 780
 tttctaagag gagtcttgcc aagaactgta tgtccaaaac tgatctgttt taacagttag 840
 tgaggaacag cttccgagat aaagtaagtt cttttttcta ttgctaattt tgctttttta 900
 aatagcagtg ttgtaagact aatattttcca cttaccacca atagagggag cattaattaa 960

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ctatgtcatg gaattgtttt gatatttttg aaaacaagtg attccaccca taaaatgaaa 1020
agagaagatt gaccttaaga aaaaaactct taaagctagg agacaatgac atgaaatcac 1080
tcaatacatg ttacaaatga aagaaggcca aaagccactt taaaatattt taaactgttt 1140
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taccgcctga aaagttgatc ttaggtgcc ttagggcca cgtgtagctt tctgtttctc 1260
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aatttttctt tattacatgc caatatTTgt acaaaaaggg cccccaatg tgtgaaatat 2280
aatcctaaaa aagaaaataa ttggaacaca tggatctgtt acaattctac acagggggaa 2340
acaagctaag c 2351

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<210> 327
<211> 97
<212> PRT
<213> Homo sapiens
<400> 327

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Met Asp Gln Pro Gly Leu His Ser Ser Arg His Ile Pro Thr Val His
 1 5 10 15

Leu Ser Phe Pro Asn Met Ser His Ser Lys Ile Val Asp Lys Leu Phe
 20 25 30

Cys Gly Lys Arg Lys Lys Leu Asp Trp Ser Gly Arg Ser Asn Leu Glu
 35 40 45

Glu Gln Arg Gly Ser Cys Leu Leu Leu Cys Ser Trp Pro Ile Lys Trp
 50 55 60

Pro Leu Ser Lys Leu Thr His Ile Leu Gly Asn Lys Pro Ile Trp Thr
 65 70 75 80

Cys Phe Lys Arg Ile Glu Met Leu Leu Asp Cys Gln Phe Ser Leu Leu
 85 90 95

Ser

<210> 328
 <211> 400
 <212> DNA
 <213> Homo sapiens

<400> 328
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 ggattccgcc cttcgtcctt gccacccgct cgccactctt ccctaatacgc tgttcattct 180
 ccggtgcgct gtcccgccat ggtctgaccc cacttcaatc ttaccttcgg tccgtccttt 240
 gaacaccccg acccccgacc cttttcttcc aaaacattcc atccttcttg gcttctgcta 300
 ctcaataatg gacagcagct cgaaggccat gtatcccacg gctttgctga aatttgtctc 360
 gggttgccct taagagactg gtcgtttcct tttgaagaga 400

<210> 329
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 329

Gly Arg Ala Cys Leu Pro His Leu Val Arg Ala Cys Asp Leu Thr Arg
1 5 10 15

Pro Ala Ala Gly Arg Cys Ile Arg Ala Val Gly Leu Leu Ser Val Arg
20 25 30

Phe Pro Pro Ala Ala Pro Ala Gly Ile Pro Pro Phe Val Leu Ala Thr
35 40 45

Arg Ser Pro Leu Phe Pro Asn Arg Cys Ser Phe Ser Gly Ala Leu Ser
50 55 60

Arg His Gly Leu Thr Pro Leu Gln Ser Tyr Leu Arg Ser Val Leu
65 70 75

<210> 330
<211> 1618
<212> DNA
<213> Homo sapiens

<400> 330
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tctagacaag atgctggaaa gaccacagga agacacagat atgtgtgcct ttattagcgg 180
agccactact tgaggagat gaagcgggag gagtgggtgg acccaatgcc aggcggccg 240
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ttgggaggga tgatcatatc gcgcaggtgc gtcttcacca cttcctgctt ctctatggtc 420
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tccgtaagtg ccagagtcct tcacatatgg attttaacct aattctgtaa tgattttaat 720
tagctgatat attaaaaaca acgtcagtaa gttttccct tcaaggaagc ctcaactttg 780
agaaacggtg aattacgtga ggtgaacctc gtatttatgt gaggaaagct ctgcactggt 840
tttgattctc acattttaat tagctgatac attaaaaaca atataagtaa tttttccctt 900

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ccgggaaacc tcaacttgga gtaacgctgg attacgtgag ctaaacctcg taattatgtg 960
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aaatacaaaa tcagctgggt gtggtggtgg gtacctgtaa tcccagctac tcgggaagtt 1500
gaggcaggaa aatcgcttga acctggaggc agaggttgcg gtgagccaag atggcgccac 1560
tgactccag cctgggtgac agagcgagac cccgtcacca aaaaaaaaaa aaaaaaaa 1618

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<210> 331
<211> 43
<212> PRT
<213> Homo sapiens

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<400> 331

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Met Arg Leu Glu Pro Gln His Ser Ala Thr Gly Arg Gly Ser Ala Ala
1           5           10           15

```

```

Ala Ala Gly Ala Arg Arg Thr Ala Ala Ser Ala Ala Gln Arg Thr Cys
20           25           30

```

```

Pro Ala Ala Gly Pro Gly Pro His Arg Gly Arg
35           40

```

```

<210> 332
<211> 3673
<212> DNA
<213> Homo sapiens

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<400> 332
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tcgccgaccc gaggtttcgg cgcgactggt tccgcatecc ctccccgccg gccgaatctg 180

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caggccccgc ggcgcaggca ggcttcgcgg ctgcgcccc	ggcccgcgca ggacctgcct	240
tgtccaccat gaaaggcacc cgggccatcg gcagcgtccc	ggagcgcagc ccagcaggtg	300
tggacctgag tctgacaggt ctccctccgc ctgtgtcccg	gcgtcctggc agtgccgcca	360
ccaccaagcc catcgtccgc tctgtctccg tggtcacagg	cagcgcagcag aagaggaagg	420
tgctggaggc cacagggcct gggggctccc aggccatcaa	caaccttaga agatccaaca	480
gcaccaagca ggtcagccag cctcggagcg gctccccag	gccaacggag cccacagact	540
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ccccagcga gaaggagcc acctggaacg tcctggatga	ccagccccgg ggcttcacct	660
tgccatcaa tgccggagt tcagtgccc ttgactcacc	agcggggccg cggaggaaa	720
aatgcaccgt ggccctggcc cccaacttca ctgctaacaa	caggagcaac aaggagcag	780
tgggcaactg cgtcaccacc atggtgcaca accgctacac	ccctcggag agggcgcctc	840
cgtcaagag ctccaaccag actgccccct cctcaacaa	catcatcaag gcagccacct	900
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gggacaacct ggagatgatg gccccgagca gggggagcgc	caagtccagg gggccactgg	1620
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 ccgttggtttt cag 3673

<210> 333
 <211> 1165
 <212> PRT
 <213> Homo sapiens
 <400> 333

Arg Ala Gly Glu Val Val Pro Gly Trp Leu Leu Ala Ala Ala Ala Ala
 1 5 10 15

His Pro Gly Arg Pro Ala Ala Ser Leu Ser Pro Gly Leu Gly Ala Val
 20 25 30

Leu Gly Val Ala Gly Arg Gln Val Ala Asp Pro Arg Phe Arg Arg Asp
 35 40 45

Trp Phe Arg Ile Pro Ser Pro Pro Ala Glu Ser Ala Gly Pro Ala Arg
 50 55 60

Gln Ala Gly Phe Ala Ala Ala Pro Pro Ala Arg Ala Gly Pro Ala Leu
 65 70 75 80

Ser Thr Met Lys Gly Thr Arg Ala Ile Gly Ser Val Pro Glu Arg Ser
 85 90 95

Pro Ala Gly Val Asp Leu Ser Leu Thr Gly Leu Pro Pro Pro Val Ser
 100 105 110

Arg Arg Pro Gly Ser Ala Ala Thr Thr Lys Pro Ile Val Arg Ser Val
 115 120 125

Ser Val Val Thr Gly Ser Glu Gln Lys Arg Lys Val Leu Glu Ala Thr
 130 135 140

Gly Pro Gly Gly Ser Gln Ala Ile Asn Asn Leu Arg Arg Ser Asn Ser
 145 150 155 160

Thr Thr Gln Val Ser Gln Pro Arg Ser Gly Ser Pro Arg Pro Thr Glu
 165 170 175

Pro Thr Asp Phe Leu Met Leu Phe Glu Gly Ser Pro Ser Gly Lys Lys
180 185 190

Arg Pro Ala Ser Leu Ser Thr Ala Pro Ser Glu Lys Gly Ala Thr Trp
195 200 205

Asn Val Leu Asp Asp Gln Pro Arg Gly Phe Thr Leu Pro Ser Asn Ala
210 215 220

Arg Ser Ser Ser Ala Leu Asp Ser Pro Ala Gly Pro Arg Arg Lys Glu
225 230 235 240

Cys Thr Val Ala Leu Ala Pro Asn Phe Thr Ala Asn Asn Arg Ser Asn
245 250 255

Lys Gly Ala Val Gly Asn Cys Val Thr Thr Met Val His Asn Arg Tyr
260 265 270

Thr Pro Ser Glu Arg Ala Pro Pro Leu Lys Ser Ser Asn Gln Thr Ala
275 280 285

Pro Ser Leu Asn Asn Ile Ile Lys Ala Ala Thr Cys Glu Gly Ser Glu
290 295 300

Ser Ser Gly Phe Gly Lys Leu Pro Lys Asn Val Ser Ser Ala Thr His
305 310 315 320

Ser Ala Arg Asn Asn Thr Gly Gly Ser Thr Gly Leu Pro Arg Arg Lys
325 330 335

Glu Val Thr Glu Glu Glu Ala Glu Arg Phe Ile His Gln Val Asn Gln
340 345 350

Ala Ala Val Thr Ile Gln Arg Trp Tyr Arg His Gln Val Gln Arg Arg
355 360 365

Gly Ala Gly Ala Ala Arg Leu Glu His Leu Leu Gln Ala Lys Arg Glu
370 375 380

Glu Gln Arg Gln Arg Ser Gly Glu Gly Thr Leu Leu Asp Leu His Gln
385 390 395 400

Gln Lys Glu Ala Ala Arg Arg Lys Ala Arg Glu Glu Lys Ala Arg Gln
 405 410 415
 Ala Arg Arg Ala Ala Ile Gln Glu Leu Gln Gln Lys Arg Ala Leu Arg
 420 425 430
 Ala Gln Lys Ala Ser Thr Ala Glu Arg Gly Pro Pro Glu Asn Pro Arg
 435 440 445
 Glu Thr Arg Val Pro Gly Met Arg Gln Pro Ala Gln Glu Leu Ser Pro
 450 455 460
 Thr Pro Gly Gly Thr Ala His Gln Ala Leu Lys Ala Asn Asn Ala Gly
 465 470 475 480
 Gly Gly Leu Pro Ala Ala Gly Pro Gly Asp Arg Cys Leu Pro Thr Ser
 485 490 495
 Asp Ser Ser Pro Glu Pro Gln Gln Pro Pro Glu Asp Arg Thr Gln Asp
 500 505 510
 Val Leu Ala Gln Asp Ala Ala Gly Asp Asn Leu Glu Met Met Ala Pro
 515 520 525
 Ser Arg Gly Ser Ala Lys Ser Arg Gly Pro Leu Glu Glu Leu Leu His
 530 535 540
 Thr Leu Gln Leu Leu Glu Lys Glu Pro Asp Ala Leu Pro Arg Pro Arg
 545 550 555 560
 Thr His His Arg Gly Arg Tyr Ala Trp Ala Ser Glu Val Thr Thr Glu
 565 570 575
 Asp Asp Ala Ser Ser Leu Thr Ala Asp Asn Leu Glu Lys Phe Gly Lys
 580 585 590
 Leu Ser Ala Phe Pro Glu Pro Pro Glu Asp Gly Thr Leu Leu Ser Glu
 595 600 605
 Ala Lys Leu Gln Ser Ile Met Ser Phe Leu Asp Glu Met Glu Lys Ser
 610 615 620

Gly Gln Asp Gln Leu Asp Ser Gln Gln Glu Gly Trp Val Pro Glu Ala
 625 630 635 640
 Gly Pro Gly Pro Leu Glu Leu Gly Ser Glu Val Ser Thr Ser Val Met
 645 650 655
 Arg Leu Lys Leu Glu Val Glu Glu Lys Lys Gln Ala Met Leu Leu Leu
 660 665 670
 Gln Arg Ala Leu Ala Gln Gln Arg Asp Leu Thr Ala Arg Arg Val Lys
 675 680 685
 Glu Thr Glu Lys Ala Leu Ser Arg Gln Leu Gln Arg Gln Arg Glu His
 690 695 700
 Tyr Glu Ala Thr Ile Gln Arg His Leu Ala Phe Ile Asp Gln Leu Ile
 705 710 715 720
 Glu Asp Lys Lys Val Leu Ser Glu Lys Cys Glu Ala Val Val Ala Glu
 725 730 735
 Leu Lys Gln Glu Asp Gln Arg Cys Thr Glu Arg Val Ala Gln Ala Gln
 740 745 750
 Ala Gln His Glu Leu Glu Ile Lys Lys Leu Lys Glu Leu Met Ser Ala
 755 760 765
 Thr Glu Lys Ala Arg Arg Glu Lys Trp Ile Ser Glu Lys Thr Lys Lys
 770 775 780
 Ile Lys Glu Val Thr Val Arg Gly Leu Glu Pro Glu Ile Gln Lys Leu
 785 790 795 800
 Ile Ala Arg His Lys Gln Glu Val Arg Arg Leu Lys Ser Leu His Glu
 805 810 815
 Ala Glu Leu Leu Gln Ser Asp Glu Arg Ala Ser Gln Arg Cys Leu Arg
 820 825 830
 Gln Ala Glu Glu Leu Arg Glu Gln Leu Glu Arg Glu Lys Glu Ala Leu
 835 840 845

Gly Gln Gln Glu Arg Glu Arg Ala Arg Gln Arg Phe Gln Gln His Leu
 850 855 860
 Glu Gln Glu Gln Trp Ala Leu Gln Gln Gln Arg Gln Arg Leu Tyr Ser
 865 870 875 880
 Glu Val Ala Glu Glu Arg Glu Arg Leu Gly Gln Gln Ala Ala Arg Gln
 885 890 895
 Arg Ala Glu Leu Glu Glu Leu Arg Gln Gln Leu Glu Glu Ser Ser Ser
 900 905 910
 Ala Leu Thr Arg Ala Leu Arg Ala Glu Phe Glu Lys Gly Arg Glu Glu
 915 920 925
 Gln Glu Arg Arg His Gln Met Glu Leu Asn Thr Leu Lys Gln Gln Leu
 930 935 940
 Glu Leu Glu Arg Gln Ala Trp Glu Ala Gly Arg Thr Arg Lys Glu Glu
 945 950 955 960
 Ala Trp Leu Leu Asn Arg Glu Gln Glu Leu Arg Glu Glu Ile Arg Lys
 965 970 975
 Gly Arg Asp Lys Glu Ile Glu Leu Val Ile His Arg Leu Glu Ala Asp
 980 985 990
 Met Ala Leu Ala Lys Glu Glu Ser Glu Lys Ala Ala Glu Ser Arg Ile
 995 1000 1005
 Lys Arg Leu Arg Asp Lys Tyr Glu Ala Glu Leu Ser Glu Leu Glu
 1010 1015 1020
 Gln Ser Glu Arg Lys Leu Gln Glu Arg Cys Ser Glu Leu Lys Gly
 1025 1030 1035
 Gln Leu Gly Glu Ala Glu Gly Glu Asn Leu Arg Leu Gln Gly Leu
 1040 1045 1050
 Val Arg Gln Lys Glu Arg Ala Leu Glu Asp Ala Gln Ala Val Asn
 1055 1060 1065

Gln Gln Leu Ser Ser Glu Arg Ser Asn Leu Ala Gln Val Ile Arg
1070 1075 1080

Gln Glu Phe Glu Asp Arg Leu Ala Ala Ser Glu Glu Glu Thr Arg
1085 1090 1095

Gln Ala Lys Ala Glu Leu Ala Thr Leu Gln Ala Arg Gln Gln Leu
1100 1105 1110

Glu Leu Glu Glu Val His Arg Arg Val Lys Thr Ala Leu Ala Arg
1115 1120 1125

Lys Glu Glu Ala Val Ser Ser Leu Arg Thr Gln His Glu Ala Ala
1130 1135 1140

Val Lys Arg Ala Asp His Leu Glu Glu Leu Leu Glu Gln His Arg
1145 1150 1155

Arg Pro Thr Pro Ser Thr Lys
1160 1165

<210> 334

<211> 1183

<212> DNA

<213> Homo sapiens

<400> 334

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atcaatcaat gtgtaaacct attactggga ctattaatga tttgaatcag caagtgtgga      180
cccttcaggg tcagaacctt gtggcagttc cacgaagtga cagtgtgacc ccagtcactg      240
ttgctgttat cacatgcaag tatccagagg ctcttgagca aggcagaggg gatcccattt      300
at ttgggaat ccagaatcca gaaatgtggt tgtattgtga gaagggttga gaacagccca      360
cattgcagct aaaagagcag aagatcatgg atctgtatgg ccaacccgag cccgtgaaac      420
ccttcctttt ctaccgtgcc aagactggta ggacctccac ccttgagtct gtggccttcc      480
cggactgggt cattgcctcc tccaagagag accagcccat cattctgact tcagaacttg      540
ggaagtcata caaactgcc tttgaattaa atataaatga ctgaactcag cctagagggt      600
gcagcttggt ctttgtctta aagttttctg ttcccaatgt gttttcgtct acattttctt      660

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agtgtcattt tcacgctggt gctgagacag gggcaaggct gctgttatca tctcatttta 720
taatgaagaa gaagcaatta cttcatagca actgaagaac aggatgtggc ctcaagaagca 780
ggagagctgg gtggtataag gctgtcctct caagctgggtg ctgtgtaggc cacaagggcat 840
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taattcttgt gttaagttaa atcatttttg tcctaattgt aatgtgtaat cttaaagtta 1140
aataaacttt gtgtatttat ataataaaaa aaaaaaaaaa aaa 1183

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<210> 335
<211> 169
<212> PRT
<213> Homo sapiens
<400> 335

```

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Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr
1          5          10          15

```

```

Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln
          20          25          30

```

```

Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Ser
          35          40          45

```

```

Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro
          50          55          60

```

```

Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
          65          70          75          80

```

```

Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr
          85          90          95

```

```

Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu
          100          105          110

```

```

Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser
          115          120          125

```

Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys
130 135 140

Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser Tyr Asn
145 150 155 160

Thr Ala Phe Glu Leu Asn Ile Asn Asp
165

<210> 336
<211> 129
<212> DNA
<213> Homo sapiens

<400> 336
tatacggctg cgagaagacg acagaaggga tacacaacca gatatttcca ggaaggaaag 60
tggaagcccc tgctaacagg tatagtctta agggagacaa aaaaaaaaaa aaaaaaaaaa 120
aagtcgtat 129

<210> 337
<211> 42
<212> PRT
<213> Homo sapiens

<400> 337

Tyr Gly Cys Glu Lys Thr Thr Glu Gly Ile His Asn Gln Ile Phe Pro
1 5 10 15

Gly Arg Lys Val Glu Ser Pro Ala Asn Arg Tyr Ser Leu Lys Gly Asp
20 25 30

Lys Lys Lys Lys Lys Lys Lys Lys Val Val
35 40

<210> 338
<211> 694
<212> DNA
<213> Homo sapiens

<400> 338
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tgcccagctt ctcccacacc actcattaca agctcacttt agaccccgat tccatcctct 180

```

tcctacagtc atcatagtga atctgctgtg gtttattcat ctctgtgtgag ttgttttagca 240
tttttaacag gtgtgctttg ttcttatacct aatccaaatg aggacaagtg cccaggaaat 300
tacacaaacc cattgaaagt tcagacggtt ataatccttg ggaaagttat tttgtggatt 360
ctccatttac tccttgaatg ctacatccag tatcaccaca gcaaaatcag aaaccgaggc 420
tataacttga tctaccgatc aacaaggcat ctcaagagac ttgcgttgat gatacagtcc 480
tctggcaaca cagtgccttct ctcatactg tgcatgcagc actccttccc agagcctggc 540
agattgtatc ttgacctcat tctggccatc ttggcactgg aactcatctg ttccctgata 600
tgtctcctca ttacacagt gaaaatccgg agatttaata aagctaaacc agagcctgat 660
atacttgacg aagacaacat ctatgcttac ccca 694

```

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<210> 339
<211> 127
<212> PRT
<213> Homo sapiens

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<400> 339

```

```

Leu Lys Val Gln Thr Val Ile Ile Leu Gly Lys Val Ile Leu Trp Ile
1           5           10           15

```

```

Leu His Leu Leu Leu Glu Cys Tyr Ile Gln Tyr His His Ser Lys Ile
20           25           30

```

```

Arg Asn Arg Gly Tyr Asn Leu Ile Tyr Arg Ser Thr Arg His Leu Lys
35           40           45

```

```

Arg Leu Ala Leu Met Ile Gln Ser Ser Gly Asn Thr Val Leu Leu Leu
50           55           60

```

```

Ile Leu Cys Met Gln His Ser Phe Pro Glu Pro Gly Arg Leu Tyr Leu
65           70           75           80

```

```

Asp Leu Ile Leu Ala Ile Leu Ala Leu Glu Leu Ile Cys Ser Leu Ile
85           90           95

```

```

Cys Leu Leu Ile Tyr Thr Val Lys Ile Arg Arg Phe Asn Lys Ala Lys
100          105          110

```

```

Pro Glu Pro Asp Ile Leu Asp Glu Asp Asn Ile Tyr Ala Tyr Pro
115          120          125

```


<210> 340
 <211> 2974
 <212> DNA
 <213> Homo sapiens

<400> 340
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 tctccctcgg cccctcccca cagatgggtgc atcccttggc agaggctcct gctcacagcc 180
 tcacttctaa ccttctggaa cccgccacc actgccaaagc tcactattga atccacgccg 240
 ttcaatgtcg cagaggggaa ggaggtgctt ctacttgtcc acaatctgcc ccagcatctt 300
 tttggctaca gctggtacaa aggtgaaaga gtggatggca accgtcaaata tataggatat 360
 gtaataggaa ctcaacaagc taccacaggg cccgcataca gtggctcgaga gataatatac 420
 cccaatgcat ccctgctgat ccagaacatc atccagaatg acacaggatt ctacacccta 480
 cacgtcataa agtcagatct tgtgaatgaa gaagcaactg gccagttccg ggtatacccg 540
 gagctgcccc agccctccat ctccagcaac aactccaaac ccgtggagga caaggatgct 600
 gtggccttca cctgtgaacc tgagactcag gacgcaacct acctgtgggtg ggtaaacaat 660
 cagagcctcc cggtcagtcc caggctgcag ctgtccaatg gcaacaggac cctcactcta 720
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 aactcagaca ctggcctcaa taggaccaca gtcacgacga tcacagtcta tgcagagcca 1080
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 ccacctgcac agtattcttg gctgattgat gggaacatcc agcaacacac acaagagctc 1500

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aaatatactt ttgtgaacaa aaattgagac atttacattt tctccctatg tggctgctcc 2880
agacttgga aactattcat gaatatttat attgtatggt aatatagtta ttgcacaagt 2940
tcaataaaaa tctgctcttt gtataacaga aaaa 2974

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<210> 341
<211> 702
<212> PRT
<213> Homo sapiens

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<400> 341

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
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Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
20 25 30

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
35 40 45

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
50 55 60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65 70 75 80

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
85 90 95

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
100 105 110

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
115 120 125

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
130 135 140

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145 150 155 160

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
165 170 175

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
180 185 190

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
195 200 205

Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
210 215 220

Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
 245 250 255
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
 290 295 300
 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
 325 330 335
 Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
 355 360 365
 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
 370 375 380
 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
 385 390 395 400
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
 420 425 430
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 435 440 445

Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 450 455 460
 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 465 470 475 480
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
 500 505 510
 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 660 665 670

37.6

Met Pro Thr Leu Leu Pro Lys Thr Ser Leu Ser Asp Leu Arg Ser Ile
 1 5 10 15

Val Lys Ser Gly Phe Pro Ala Cys His Gly Lys Leu Leu Ala Thr Trp
 20 25 30

Glu

<210> 344
 <211> 644
 <212> DNA
 <213> Homo sapiens

<400> 344
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 cgcattgagt cggagtggag cacagaagt taggtccttt tgcgctgttt caagctaaac 180
 ccgtgtcact gatgccgtac agaagttaca gaatgggacg ccaccccaaa cattacgtca 240
 tccgctgacc atttccttgc ggtcttccca ccgtctaaat cgccatataa tctgatggat 300
 ggggtcctcg cgcggttcag ctctgggag acagcgtaac ccgtcgctcc tccctctgag 360
 ggagggcggtg gacggggcac gggatttga gcggtgaagg aatcgggacc gaaaggagtc 420
 ccaggacacc ggaaccagga ctcccggcg caccggaga gtttcgagc tcctttgaag 480
 tatgaatcag aacttctgga tgggaatcct ggagccacca cttgccctat ggtcgcaatg 540
 ggcaagtcgc tcaacctccc agatcctgtt ttctcatgag taaaacgggg attataatac 600
 ccacctgaca atattatctt tgtgagaatt aaatgagtta gaat 644

<210> 345
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 345

Met Gly Ser Ser Arg Gly Ser Ala Pro Gly Arg Gln Arg Asn Pro Ser
 1 5 10 15

Leu Leu Pro Leu Arg Glu Gly Val Asp Gly Ala Arg Asp Leu Glu Arg
 20 25 30

Gly Arg Asn Arg Asp Arg Lys Glu Ser Gln Asp Thr Gly Thr Arg Thr
 35 40 45

Pro Arg Arg Thr Arg Arg Val Ser Glu Leu Leu
 50 55

<210> 346
 <211> 2373
 <212> DNA
 <213> Homo sapiens

<400> 346
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 atgcagctca gctgggacat caacgatccg cagatgcctc aggagctggc cctctttgac 180
 caattccgag agtggcctga cggctatgtg cgcttcatct acagcagcga tgagaagaag 240
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 gaaaatcaag acagcagtgg tcatttcagc aacatacctc ccttggaata tccagaagac 720
 tttgatatag ttactgaaac cagcttcctt attccagggc agccttgccc ttccttccca 780
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cataacctff tcataacatg atagtttcca taacagagac agcctaacaa tgatgagttg 2280
tatttaatgg attaccattg tactaaatac attttttttc tgattagggt tcagaattat 2340
aattaaaatg ttttgcttaa aaaaaaaaaa aaa 2373

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<210> 347

<211> 506

<212> PRT

<213> Homo sapiens

<400> 347

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Met Pro Ala Ala Val Gln Glu Ala Val Gly Val Cys Ser Tyr Gly
1           5           10           15

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Met Gln Leu Ser Trp Asp Ile Asn Asp Pro Gln Met Pro Gln Glu Leu
20           25           30

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Ala Leu Phe Asp Gln Phe Arg Glu Trp Pro Asp Gly Tyr Val Arg Phe
35           40           45

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Ile Tyr Ser Ser Asp Glu Lys Lys Ala Gln Arg His Leu Ser Gly Trp
 50 55 60

Ala Met Arg Asn Thr Asn Asn His Asn Gly His Ile Leu Lys Lys Ser
 65 70 75 80

Cys Leu Gly Val Val Val Cys Thr Gln Ala Cys Thr Leu Pro Asp Gly
 85 90 95

Ser Arg Leu Gln Leu Arg Pro Ala Ile Cys Asp Lys Ala Arg Leu Lys
 100 105 110

Gln Gln Lys Lys Ala Cys Pro Asn Cys His Ser Ala Leu Glu Leu Ile
 115 120 125

Pro Cys Arg Gly His Ser Gly Tyr Pro Val Thr Asn Phe Trp Arg Leu
 130 135 140

Asp Gly Asn Ala Ile Phe Phe Gln Ala Lys Gly Val His Asp His Pro
 145 150 155 160

Arg Pro Glu Ser Lys Ser Glu Thr Glu Ala Arg Arg Ser Ala Ile Lys
 165 170 175

Arg Gln Met Ala Ser Phe Tyr Gln Pro Gln Lys Lys Arg Ile Arg Glu
 180 185 190

Ser Glu Ala Glu Glu Asn Gln Asp Ser Ser Gly His Phe Ser Asn Ile
 195 200 205

Pro Pro Leu Glu Asn Pro Glu Asp Phe Asp Ile Val Thr Glu Thr Ser
 210 215 220

Phe Pro Ile Pro Gly Gln Pro Cys Pro Ser Phe Pro Lys Ser Asp Val
 225 230 235 240

Tyr Lys Ala Thr Cys Asp Leu Ala Thr Phe Gln Gly Asp Lys Met Pro
 245 250 255

Pro Phe Gln Lys Tyr Ser Ser Pro Arg Ile Tyr Leu Pro Arg Pro Pro
 260 265 270

Cys Ser Tyr Glu Leu Ala Asn Pro Gly Tyr Thr Asn Ser Ser Pro Tyr
 275 280 285
 Pro Thr Leu Tyr Lys Asp Ser Thr Ser Ile Pro Asn Asp Thr Asp Trp
 290 295 300
 Val His Leu Asn Thr Leu Gln Cys Asn Val Asn Ser Tyr Ser Ser Tyr
 305 310 315 320
 Glu Arg Ser Phe Asp Phe Thr Asn Lys Gln His Gly Trp Lys Pro Ala
 325 330 335
 Leu Gly Lys Pro Ser Leu Val Glu Arg Thr Asn His Gly Gln Phe Gln
 340 345 350
 Ala Met Ala Thr Arg Pro Tyr Tyr Asn Pro Glu Leu Pro Cys Arg Tyr
 355 360 365
 Leu Thr Thr Pro Pro Pro Gly Ala Pro Ala Leu Gln Thr Val Ile Thr
 370 375 380
 Thr Thr Thr Lys Val Ser Tyr Gln Ala Tyr Gln Pro Pro Ala Met Lys
 385 390 395 400
 Tyr Ser Asp Ser Val Arg Glu Val Lys Ser Leu Ser Ser Cys Asn Tyr
 405 410 415
 Ala Pro Glu Asp Thr Gly Met Ser Val Tyr Pro Glu Pro Trp Gly Pro
 420 425 430
 Pro Val Thr Val Thr Arg Ala Ala Ser Pro Ser Gly Pro Pro Pro Met
 435 440 445
 Lys Ile Ala Gly Asp Cys Arg Ala Ile Arg Pro Thr Val Ala Ile Pro
 450 455 460
 His Glu Pro Val Ser Ser Arg Thr Asp Glu Ala Glu Thr Trp Asp Val
 465 470 475 480
 Cys Leu Ser Gly Leu Gly Ser Ala Val Ser Tyr Ser Asp Arg Val Gly
 485 490 495

Pro Phe Phe Thr Tyr Asn Asn Glu Asp Phe
500 505

<210> 348
<211> 428
<212> DNA
<213> Homo sapiens

<400> 348
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 ctctaccac tcctaccacc aagtccctta ttggtctcc tggttaactg gggaaaggga 180
 ggatccttta actttttacc actgtcctta ctatttctga gttctcttat ctataatctg 240
 tcttatgtcc tatagcacia atcactttat atattgcttt cccctcagca aactcctact 300
 ttccattctg agtttcaact tcagtttatg ccataatcta agccacttcc ctgctcttct 360
 ctttaaccag actcatcttc ttataacctg ctagaacaca ggcttctgag aacaggaatc 420
 accatcag 428

<210> 349
<211> 42
<212> PRT
<213> Homo sapiens

<400> 349

Met Ser Tyr Ser Thr Asn His Phe Ile Tyr Cys Phe Pro Leu Ser Lys
1 5 10 15

Leu Leu Leu Phe Ile Leu Ser Phe Asn Phe Ser Leu Cys His Asn Leu
20 25 30

Ser His Phe Pro Ala Leu Leu Phe Asn Gln
35 40

<210> 350
<211> 1875
<212> DNA
<213> Homo sapiens

<400> 350
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tttgtccggg agcctgggtct tcccgtcctt gggctgacag gtgctgctgc ctctgagccc	180
tccctgctaa gagctgtgtg ctgggtaagg ctgggtggccc tttgggctcc ctgtccagga	240
tttgtgctct ggagggtagg gcttgctggg ctggggactg gaggggaacg tggagctcct	300
tctgcctcct ttctgcccc atgacagcag gcagatccca ggagagaaga gctcaggaga	360
tgggaagagg atctgtccag gggttagacc tcaagggtga cttggagttc tttacggcac	420
ccatgctttc tttgaggagt tttgtgtttg tgggtgtggg gtccggggctc acctcctccc	480
acatccctgc ccagagggtg gcagagtggg ggcagtgcct tgctccccct gctcgtcttc	540
tgctgacctc cggctccctg tgctgcccc ggaccatgaa tggcacctac aacacctgtg	600
gctccagcga cctcacctgg cccccagcga tcaagctggg cttctacgcc tacttgggcg	660
tcctgctggt gctaggcctg ctgctcaaca gcctggcgct ctgggtgttc tgctgccgca	720
tgcagcagtg gacggagacc cgcactaca tgaccaacct ggcggtggcc gacctctgcc	780
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ccccaggca ggtgcggcc gtgtgcgagg tcctctgggt gctggtcac ggtccctgg	1020
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tccccaccca gagtc 1875

<210> 351

<211> 309

<212> PRT

<213> Homo sapiens

<400> 351

Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser Asp Leu Thr Trp Pro
1 5 10 15

Pro Ala Ile Lys Leu Gly Phe Tyr Ala Tyr Leu Gly Val Leu Leu Val
20 25 30

Leu Gly Leu Leu Leu Asn Ser Leu Ala Leu Trp Val Phe Cys Cys Arg
35 40 45

Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val
50 55 60

Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe Val Leu His Ser Leu
65 70 75 80

Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly Ile Tyr
85 90 95

Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val
100 105 110

Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg
115 120 125

Ser Pro Arg Gln Ala Ala Ala Val Cys Ala Val Leu Trp Val Leu Val
130 135 140

Ile Gly Ser Leu Val Ala Arg Trp Leu Leu Gly Ile Gln Glu Gly Gly
145 150 155 160

Phe Cys Phe Arg Ser Thr Arg His Asn Phe Asn Ser Met Ala Phe Pro
165 170 175

Leu Leu Gly Phe Tyr Leu Pro Leu Ala Val Val Val Phe Cys Ser Leu
 180 185 190
 Lys Val Val Thr Ala Leu Ala Gln Arg Pro Pro Thr Asp Val Gly Gln
 195 200 205
 Ala Glu Ala Thr Arg Lys Ala Ala Arg Met Val Trp Ala Asn Leu Leu
 210 215 220
 Val Phe Val Val Cys Phe Leu Pro Leu His Val Gly Leu Thr Val Arg
 225 230 235 240
 Leu Ala Val Gly Trp Asn Ala Cys Ala Leu Leu Glu Thr Ile Arg Arg
 245 250 255
 Ala Leu Tyr Ile Thr Ser Lys Leu Ser Asp Ala Asn Cys Cys Leu Asp
 260 265 270
 Ala Ile Cys Tyr Tyr Tyr Met Ala Lys Glu Phe Gln Glu Ala Ser Ala
 275 280 285
 Leu Ala Val Ala Pro Ser Ala Lys Ala His Lys Ser Gln Asp Ser Leu
 290 295 300
 Cys Val Thr Leu Ala
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<210> 352
 <211> 1803
 <212> DNA
 <213> Homo sapiens

<400> 352
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 taccctatta ccaaagaggc acttgaggaa acacgacttg ggaagctcat caacgacgtc 180
 cgcaagaaaa ccaagaacga ggagctcgcc aagcggggcca agaagctgct gcggagctgg 240
 cagaagctca tcgagccggc acaccagcat gaggcggcgc tgcgggggct ggcggggggc 300
 accggctctg ccaacggggg cgcacacaac tgccggccgg aggtgggggc ggctggccca 360
 cccaggagca tccatgacct gaagagccgc aatgacctcc agaggctgcc cgggcagcgg 420

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cccaccaacg ggatcagtgg gagtccagag agcttcgcca gtcacctgga tggcagtggg 600
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cctggtctga cccgggaggt cacacaggac gatctcgaca gaatccaggc cagccagtgg 1680
ccgggggtga acgggtgtca ggacacacag ggtaactgg atgactggac gcagtgcata 1740
tcgctcgatc cgcacggcga cgacgggcgc ttgaacattc tgccttatgt ctgcttgac 1800
tga 1803

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<210> 353
<211> 600
<212> PRT
<213> Homo sapiens
<400> 353

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Met Thr Ala Ala Pro Ala Ser Pro Gln Gln Ile Arg Asp Arg Leu Leu
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 Gln Ala Ile Asp Pro Gln Ser Asn Ile Arg Asn Met Val Ala Val Leu
 20 25 30
 Glu Val Ile Ser Ser Leu Glu Lys Tyr Pro Ile Thr Lys Glu Ala Leu
 35 40 45
 Glu Glu Thr Arg Leu Gly Lys Leu Ile Asn Asp Val Arg Lys Lys Thr
 50 55 60
 Lys Asn Glu Glu Leu Ala Lys Arg Ala Lys Lys Leu Leu Arg Ser Trp
 65 70 75 80
 Gln Lys Leu Ile Glu Pro Ala His Gln His Glu Ala Ala Leu Arg Gly
 85 90 95
 Leu Ala Gly Ala Thr Gly Ser Ala Asn Gly Gly Ala His Asn Cys Arg
 100 105 110
 Pro Glu Val Gly Ala Ala Gly Pro Pro Arg Ser Ile His Asp Leu Lys
 115 120 125
 Ser Arg Asn Asp Leu Gln Arg Leu Pro Gly Gln Arg Leu Asp Arg Leu
 130 135 140
 Gly Ser Arg Lys Arg Arg Gly Asp Gln Arg Asp Phe Gly His Pro Gly
 145 150 155 160
 Pro Pro Pro Lys Val Ser Lys Ala Ser His Asp Pro Leu Val Pro Asn
 165 170 175
 Ser Ser Pro Leu Pro Thr Asn Gly Ile Ser Gly Ser Pro Glu Ser Phe
 180 185 190
 Ala Ser Ser Leu Asp Gly Ser Gly His Ala Gly Pro Glu Gly Ser Arg
 195 200 205
 Leu Glu Arg Asp Glu Asn Asp Lys His Ser Gly Lys Ile Pro Val Asn
 210 215 220

Ala Val Arg Pro His Thr Ser Ser Pro Gly Leu Gly Lys Pro Pro Gly
225 230 235 240

Pro Cys Leu Gln Pro Lys Ala Ser Val Leu Gln Gln Leu Asp Arg Val
245 250 255

Asp Glu Thr Pro Gly Pro Pro His Pro Lys Gly Pro Pro Arg Cys Ser
260 265 270

Phe Ser Pro Arg Asn Ser Arg His Glu Gly Ser Phe Ala Arg Gln Gln
275 280 285

Ser Leu Tyr Ala Pro Lys Gly Ser Val Pro Ser Pro Ser Pro Arg Pro
290 295 300

Gln Ala Leu Asp Ala Thr Gln Val Pro Ser Pro Leu Pro Leu Ala Gln
305 310 315 320

Pro Ser Thr Pro Pro Val Arg Arg Leu Glu Leu Leu Pro Ser Ala Glu
325 330 335

Ser Pro Val Cys Trp Leu Glu Gln Pro Glu Ser His Gln Arg Leu Ala
340 345 350

Gly Pro Gly Cys Lys Ala Gly Leu Ser Pro Ala Glu Pro Leu Leu Ser
355 360 365

Arg Ala Gly Phe Ser Pro Asp Ser Ser Lys Ala Asp Ser Asp Ala Ala
370 375 380

Ser Ser Gly Gly Ser Asp Ser Lys Lys Lys Lys Arg Tyr Arg Pro Arg
385 390 395 400

Asp Tyr Thr Val Asn Leu Asp Gly Gln Val Ala Glu Ala Gly Val Lys
405 410 415

Pro Val Arg Leu Lys Glu Arg Lys Leu Thr Phe Asp Pro Met Thr Arg
420 425 430

Gln Ile Lys Pro Leu Thr Gln Lys Glu Pro Val Arg Ala Asp Ser Pro
435 440 445

Val His Met Glu Gln Gln Ser Arg Thr Glu Leu Asp Lys Gln Glu Ala
450 455 460

Lys Ala Ser Leu Gln Ser Pro Phe Glu Gln Thr Asn Trp Lys Glu Leu
465 470 475 480

Ser Arg Asn Glu Ile Ile Gln Ser Tyr Leu Ser Arg Gln Ser Ser Leu
485 490 495

Leu Ser Ser Ser Gly Ala Gln Thr Pro Gly Ala His His Phe Met Ser
500 505 510

Glu Tyr Leu Lys Gln Glu Glu Ser Thr Arg Gln Gly Ala Arg Gln Leu
515 520 525

His Val Leu Val Pro Gln Ser Pro Pro Thr Asp Leu Pro Gly Leu Thr
530 535 540

Arg Glu Val Thr Gln Asp Asp Leu Asp Arg Ile Gln Ala Ser Gln Trp
545 550 555 560

Pro Gly Val Asn Gly Cys Gln Asp Thr Gln Gly Asn Trp Tyr Asp Trp
565 570 575

Thr Gln Cys Ile Ser Leu Asp Pro His Gly Asp Asp Gly Arg Leu Asn
580 585 590

Ile Leu Pro Tyr Val Cys Leu Asp
595 600

<210> 354

<211> 1279

<212> DNA

<213> Homo sapiens

<400> 354

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cctgtgggca tcttgactgc aattggcatg gtcctcctgg ggacccgagg agccaccgct 180

tcccagttgg aggaggtgtt tcactctgaa aaagagacga agagctcaag aataaaggct 240

gaagaaaaag aggtgattga gaacacagaa gcagtacatc aacaattcca aaagtttttg 300

actgaaataa gcaaactcac taatgattat gaactgaaca taaccaacag gctgtttgga 360
 gaaaaaacat acctcttcct tcaaaaatac ttagattatg ttgaaaaata ttatcatgca 420
 tctctggaac ctgttgattt tgtaaagca gccgatgaaa gtcgaaagaa gattaattcc 480
 tgggttgaaa gcaaaacaaa tgaaaaaatc aaggacttgt tcccagatgg ctctattagt 540
 agctctacca agctggtgct ggtgaacatg gtttatttta aagggcaatg ggacaggag 600
 ttttaagaaag aaaataactaa ggaagagaaa ttttgatga ataagagcac aagtaaactt 660
 gtacagatga tgacacagag ccattccttt agcttcactt tcctggagga cttgcaggcc 720
 aaaattctag ggattccata taaaaacaac gacctaaagca tgtttgtgct tctgccaac 780
 gacatcgatg gcctggagaa gataatagat aaaataagtc ctgagaaatt ggtagagtgg 840
 actagtccag ggcatatgga agaaagaaag gtgaatctgc acttgccccg gtttgagggtg 900
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 ccttaagatg atcgttgcca tggcattgct gcttttagca aaaaacaact accagtggta 1260
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<210> 355
 <211> 391
 <212> PRT
 <213> Homo sapiens

<400> 355

Met Asp Ser Leu Gly Ala Val Ser Thr Arg Leu Gly Phe Asp Leu Phe
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Lys Glu Leu Lys Lys Thr Asn Asp Gly Asn Ile Phe Phe Ser Pro Val
 20 25 30

Gly Ile Leu Thr Ala Ile Gly Met Val Leu Leu Gly Thr Arg Gly Ala
 35 40 45

Thr Ala Ser Gln Leu Glu Glu Val Phe His Ser Glu Lys Glu Thr Lys
 50 55 60

Ser Ser Arg Ile Lys Ala Glu Glu Lys Glu Val Ile Glu Asn Thr Glu
 65 70 75 80

Ala Val His Gln Gln Phe Gln Lys Phe Leu Thr Glu Ile Ser Lys Leu
 85 90 95

Thr Asn Asp Tyr Glu Leu Asn Ile Thr Asn Arg Leu Phe Gly Glu Lys
 100 105 110

Thr Tyr Leu Phe Leu Gln Lys Tyr Leu Asp Tyr Val Glu Lys Tyr Tyr
 115 120 125

His Ala Ser Leu Glu Pro Val Asp Phe Val Asn Ala Ala Asp Glu Ser
 130 135 140

Arg Lys Lys Ile Asn Ser Trp Val Glu Ser Lys Thr Asn Glu Lys Ile
 145 150 155 160

Lys Asp Leu Phe Pro Asp Gly Ser Ile Ser Ser Ser Thr Lys Leu Val
 165 170 175

Leu Val Asn Met Val Tyr Phe Lys Gly Gln Trp Asp Arg Glu Phe Lys
 180 185 190

Lys Glu Asn Thr Lys Glu Glu Lys Phe Trp Met Asn Lys Ser Thr Ser
 195 200 205

Lys Ser Val Gln Met Met Thr Gln Ser His Ser Phe Ser Phe Thr Phe
 210 215 220

Leu Glu Asp Leu Gln Ala Lys Ile Leu Gly Ile Pro Tyr Lys Asn Asn
 225 230 235 240

Asp Leu Ser Met Phe Val Leu Leu Pro Asn Asp Ile Asp Gly Leu Glu
 245 250 255

Lys Ile Ile Asp Lys Ile Ser Pro Glu Lys Leu Val Glu Trp Thr Ser
 260 265 270

Pro Gly His Met Glu Glu Arg Lys Val Asn Leu His Leu Pro Arg Phe
 275 280 285

Glu Val Glu Asp Ser Tyr Asp Leu Glu Ala Val Leu Ala Ala Met Gly
290 295 300

Met Gly Asp Ala Phe Ser Glu His Lys Ala Asp Tyr Ser Gly Met Ser
305 310 315 320

Ser Gly Ser Gly Leu Tyr Ala Gln Lys Phe Leu His Ser Ser Phe Val
325 330 335

Ala Val Thr Glu Glu Gly Thr Glu Ala Ala Ala Ala Thr Gly Ile Gly
340 345 350

Phe Thr Val Thr Ser Ala Pro Gly His Glu Asn Val His Cys Asn His
355 360 365

Pro Phe Leu Phe Phe Ile Arg His Asn Glu Ser Asn Ser Ile Leu Phe
370 375 380

Phe Gly Arg Phe Ser Ser Pro
385 390

<210> 356
<211> 213
<212> DNA
<213> Homo sapiens

<400> 356
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aaggttttat cttgttttat cttgttttca agacaagggtc ttgctctatc acccagattg 180
gagtacagtg gcaaggtcat agatcactgc aac 213

<210> 357
<211> 36
<212> PRT
<213> Homo sapiens

<400> 357

Met Val Asp Glu Gly Lys Val Leu Ser Cys Phe Ile Leu Phe Ser Arg
1 5 10 15

Gln Gly Leu Ala Leu Ser Pro Arg Leu Glu Tyr Ser Gly Lys Val Ile
20 25 30

Asp His Cys Asn
35

<210> 358
<211> 2356
<212> DNA
<213> Homo sapiens

<400> 358
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ggaccctgca gaacaaaagg gtgttcctgg ccaccttcgc cgcagtgtc ggcaatttca 180
gctttgggta tgccctggtc tacacatccc ctgtcatccc agccctggag cgctccttgg 240
atcctgacct gcatctgacc aaatcccagg catcctgggt tgggtccgtg ttcaccctgg 300
gagcagcggc cggaggcctg agtgccatga tcctcaacga cctcctgggc cggaagctga 360
gcatcatgtt ctcagctgtg ccgtcggcgg ccggctatgc gctcatggcg ggtgcgcacg 420
gcctctggat gctgctgtc ggaaggacgc tgacgggctt cgccgggggg ctcacagctg 480
cctgcatccc ggtgtacgtg tctgagattg ctccccagg cgttcgtggg gctctggggg 540
ccacacccca gctcatggca gtgttcggat ccctgtccct ctacgccctt ggcctcctgc 600
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<210> 359
 <211> 507
 <212> PRT
 <213> Homo sapiens

<400> 359

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```

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Pro Glu Lys Pro Pro Pro Ser Pro Gly Asp Arg Ala Arg Val Gly Thr
20          25          30

```

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Leu Gln Asn Lys Arg Val Phe Leu Ala Thr Phe Ala Ala Val Leu Gly
35          40          45

```

```

Asn Phe Ser Phe Gly Tyr Ala Leu Val Tyr Thr Ser Pro Val Ile Pro
50          55          60

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Ala Leu Glu Arg Ser Leu Asp Pro Asp Leu His Leu Thr Lys Ser Gln
65 70 75 80

Ala Ser Trp Phe Gly Ser Val Phe Thr Leu Gly Ala Ala Ala Gly Gly
85 90 95

Leu Ser Ala Met Ile Leu Asn Asp Leu Leu Gly Arg Lys Leu Ser Ile
100 105 110

Met Phe Ser Ala Val Pro Ser Ala Ala Gly Tyr Ala Leu Met Ala Gly
115 120 125

Ala His Gly Leu Trp Met Leu Leu Leu Gly Arg Thr Leu Thr Gly Phe
130 135 140

Ala Gly Gly Leu Thr Ala Ala Cys Ile Pro Val Tyr Val Ser Glu Ile
145 150 155 160

Ala Pro Pro Gly Val Arg Gly Ala Leu Gly Ala Thr Pro Gln Leu Met
165 170 175

Ala Val Phe Gly Ser Leu Ser Leu Tyr Ala Leu Gly Leu Leu Leu Pro
180 185 190

Trp Arg Trp Leu Ala Val Ala Gly Glu Ala Pro Val Leu Ile Met Ile
195 200 205

Leu Leu Leu Ser Phe Met Pro Asn Ser Pro Arg Phe Leu Leu Ser Arg
210 215 220

Gly Arg Asp Glu Glu Ala Leu Arg Ala Leu Ala Trp Leu Arg Gly Thr
225 230 235 240

Asp Val Asp Val His Trp Glu Phe Glu Gln Ile Gln Asp Asn Val Arg
245 250 255

Arg Gln Ser Ser Arg Val Ser Trp Ala Glu Ala Arg Ala Pro His Val
260 265 270

Cys Arg Pro Ile Thr Val Ala Leu Leu Met Arg Leu Leu Gln Gln Leu
275 280 285

Thr Gly Ile Thr Pro Ile Leu Val Tyr Leu Gln Ser Ile Phe Asp Ser
 290 295 300

Thr Ala Val Leu Leu Pro Pro Lys Asp Asp Ala Ala Ile Val Gly Ala
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Val Arg Leu Leu Ser Val Leu Ile Ala Ala Leu Thr Met Asp Leu Ala
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Gly Arg Lys Val Leu Leu Phe Val Ser Ala Ala Ile Met Phe Ala Ala
 340 345 350

Asn Leu Thr Leu Gly Leu Tyr Ile His Phe Gly Pro Arg Pro Leu Ser
 355 360 365

Pro Asn Ser Thr Ala Gly Leu Glu Ser Glu Ser Trp Gly Asp Leu Ala
 370 375 380

Gln Pro Leu Ala Ala Pro Ala Gly Tyr Leu Thr Leu Val Pro Leu Leu
 385 390 395 400

Ala Thr Met Leu Phe Ile Met Gly Tyr Ala Val Gly Trp Gly Pro Ile
 405 410 415

Thr Trp Leu Leu Met Ser Glu Val Leu Pro Leu Arg Ala Arg Gly Val
 420 425 430

Ala Ser Gly Leu Cys Val Leu Ala Ser Trp Leu Thr Ala Phe Val Leu
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Thr Lys Ser Phe Leu Pro Val Val Ser Thr Phe Gly Leu Gln Val Pro
 450 455 460

Phe Phe Phe Phe Ala Ala Ile Cys Leu Val Ser Leu Val Phe Thr Gly
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Phe Phe Arg Thr Gly Arg Arg Ser Phe Leu Arg
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 <212> PRT
 <213> Homo sapiens

<400> 361

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Phe Phe

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 <211> 845
 <212> DNA
 <213> Homo sapiens

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<210> 363
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<212> PRT
<213> Homo sapiens

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<400> 363

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Met Pro Glu Pro Ala Lys Ser Ala Pro Ala Pro Lys Lys Gly Ser Lys
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```

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Lys Ala Val Thr Lys Ala Gln Lys Lys Asp Gly Lys Lys Arg Lys Arg
20           25           30

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```

Ser Arg Lys Glu Ser Tyr Ser Val Tyr Val Tyr Lys Val Leu Lys Gln
35           40           45

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Val His Pro Asp Thr Gly Ile Ser Ser Lys Ala Met Gly Ile Met Asn
50           55           60

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Ser Phe Val Asn Asp Ile Phe Glu Arg Ile Ala Gly Glu Ala Ser Arg
65           70           75           80

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Leu Ala His Tyr Asn Lys Arg Ser Thr Ile Thr Ser Arg Glu Ile Gln
85           90           95

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Thr Ala Val Arg Leu Leu Leu Pro Gly Glu Leu Ala Lys His Ala Val
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Ser Glu Gly Thr Lys Ala Val Thr Lys Tyr Thr Ser Ala Lys
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<210> 365
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 365

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Phe Gln His Thr Cys Leu His Leu Ser Val Pro Leu Ala Ser Cys Gly
 35 40 45

Arg Arg Gly Phe
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<210> 366
 <211> 4222
 <212> DNA
 <213> Homo sapiens

<400> 366

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<211> 197

<212> PRT

<213> Homo sapiens

<400> 367

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Leu Ser Cys Ile Pro Arg Tyr Phe Phe Leu Phe Val Ala Asn Val Asn
35 40 45

Glu Ser Ser Phe Met Ile Cys Leu Pro Ala Cys Leu Leu Phe Val His
50 55 60

Gly Asn Ala Ser Tyr Phe Cys Thr Leu Ile Leu Tyr Pro Glu Ile Leu
65 70 75 80

Leu Leu Leu Leu Ile Thr Leu Arg Ser Phe Gly Pro Glu Thr Met Arg
85 90 95

Phe Ser Arg Cys Arg Ile Arg Ser Ser Ala Asn Lys Asp Asn Leu Thr
100 105 110

Ser Ser Leu Ser Ile Arg Ile Leu Phe Ile Ser Ser Ser Gly Leu Ile
115 120 125

Phe Leu Ala Lys Ala Ser Asp Thr Ile Leu Asn Gly Ser Gly Glu Arg
130 135 140

Gly His Ser Phe Leu Val Pro Val Phe Arg Trp Asn Val Ser Ser Phe
145 150 155 160

Cys Thr Phe Ser Met Ile Leu Ala Val Gly Leu Leu Tyr Met Ala Leu
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Asn Leu Lys Glu Cys
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<211> 2406
<212> DNA
<213> Homo sapiens

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agtcacctta gtggaaaggt taaaaaccag agcctggaaa ccaagatgat tgatttgaca 1860
aggtatttta gtctagtttt atatgaacgg ttgtatcagg gtaaccaact cgatttgga 1920
tgaatcttag ggcaccaaag actaagacag tatctttaag attgctaggg aaaagggccc 1980
tatgtgtcag gcctctgagc ccaagccaag catcgcatcc cctgtgattt gcacgtatac 2040
atccagatgg cctaaagtaa ctgaagatcc acaaaagaag taaaaatagc cttaactgat 2100
gacattccac cattgtgatt tgttcctgcc ccaccctaac tgatcaatgt actttgtaat 2160
ctccccacc cttaagaagg tactttgtaa tcttccccac ccttaagaag gttctttgta 2220
attctcccca cccttgagaa tgtactttgt gagatccacc ctgccacaa aacattgctc 2280
ttaacttcac cgctaaccc aaaacctata agaactaatg ataatccatc acccttcgct 2340
gactctcttt tcggactcag cccacctgca ccaggtgaa ataaacagct ttattgctca 2400
aaaaaa 2406

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<210> 369

<211> 414

<212> PRT

<213> Homo sapiens

<400> 369

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Met Lys Ala Gln Thr Ala Leu Ser Phe Phe Leu Ile Leu Ile Thr Ser
1           5           10           15

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Leu Ser Gly Ser Gln Gly Ile Phe Pro Leu Ala Phe Phe Ile Tyr Val
          20           25           30

```

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Pro Met Asn Glu Gln Ile Val Ile Gly Arg Leu Asp Glu Asp Ile Ile
          35           40           45

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Leu Pro Ser Ser Phe Glu Arg Gly Ser Glu Val Val Ile His Trp Lys
 50 55 60
 Tyr Gln Asp Ser Tyr Lys Val His Ser Tyr Tyr Lys Gly Ser Asp His
 65 70 75 80
 Leu Glu Ser Gln Asp Pro Arg Tyr Ala Asn Arg Thr Ser Leu Phe Tyr
 85 90 95
 Asn Glu Ile Gln Asn Gly Asn Ala Ser Leu Phe Phe Arg Arg Val Ser
 100 105 110
 Leu Leu Asp Glu Gly Ile Tyr Thr Cys Tyr Val Gly Thr Ala Ile Gln
 115 120 125
 Val Ile Thr Asn Lys Val Val Leu Lys Val Gly Val Phe Leu Thr Pro
 130 135 140
 Val Met Lys Tyr Glu Lys Arg Asn Thr Asn Ser Phe Leu Ile Cys Ser
 145 150 155 160
 Val Leu Ser Val Tyr Pro Arg Pro Ile Ile Thr Trp Lys Met Asp Asn
 165 170 175
 Thr Pro Ile Ser Glu Asn Asn Met Glu Glu Thr Gly Ser Leu Asp Ser
 180 185 190
 Phe Ser Ile Asn Ser Pro Leu Asn Ile Thr Gly Ser Asn Ser Ser Tyr
 195 200 205
 Glu Cys Thr Ile Glu Asn Ser Leu Leu Lys Gln Thr Trp Thr Gly Arg
 210 215 220
 Trp Thr Met Lys Asp Gly Leu His Lys Met Gln Ser Glu His Val Ser
 225 230 235 240
 Leu Ser Cys Gln Pro Val Asn Asp Tyr Phe Ser Pro Asn Gln Asp Phe
 245 250 255
 Lys Val Thr Trp Ser Arg Met Lys Ser Gly Thr Phe Ser Val Leu Ala
 260 265 270

Tyr Tyr Leu Ser Ser Ser Gln Asn Thr Ile Ile Asn Glu Ser Arg Phe
275 280 285

Ser Trp Asn Lys Glu Leu Ile Asn Gln Ser Asp Phe Ser Met Asn Leu
290 295 300

Met Asp Leu Asn Leu Ser Asp Ser Gly Glu Tyr Leu Cys Asn Ile Ser
305 310 315 320

Ser Asp Glu Tyr Thr Leu Leu Thr Ile His Thr Val His Val Glu Pro
325 330 335

Ser Gln Glu Thr Ala Ser His Asn Lys Gly Leu Trp Ile Leu Val Pro
340 345 350

Ser Ala Ile Leu Ala Ala Phe Leu Leu Ile Trp Ser Val Lys Cys Cys
355 360 365

Arg Ala Gln Leu Glu Ala Arg Arg Ser Arg His Pro Ala Asp Gly Ala
370 375 380

Gln Gln Glu Arg Cys Cys Val Pro Pro Gly Glu Arg Cys Pro Ser Ala
385 390 395 400

Pro Asp Asn Gly Glu Glu Asn Val Pro Leu Ser Gly Lys Val
405 410

<210> 370

<211> 415

<212> DNA

<213> Homo sapiens

<400> 370

tggtacgtcg tgataccaga ttagaaaaag aactaatagc tttttttcat atatatttat	60
atataaataa ttttatagtg tgtgtattat atatcatcaa aatatatttg ataattattgt	120
gtatgttatt gtatatatta tctttttatat ataaacataa aattttacata cacaaatttt	180
attaaaatat aaatatattc attgtgtata taaaatatag ctattatata cagtatacaa	240
tttaatatagct attacggtat gcaatattac atatactgta caatttatat tgtatatatg	300
tataaataaa agacatacac atatatatat atcatgtgtt acttaatgat tgggtagtca	360
cagaccgatc cgagtagggc cagatatatc gatccctggg gtgggtagtc acaga	415

<210> 371
 <211> 22
 <212> PRT
 <213> Homo sapiens

<400> 371

Leu Gly Ser His Arg Pro Ile Arg Val Gly Pro Asp Ile Arg Ile Pro
 1 5 10 15

Gly Val Gly Ser His Arg
 20

<210> 372
 <211> 624
 <212> DNA
 <213> Homo sapiens

<400> 372
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 agacagcaaa gaggacagaa gggatcatga aaagtttctg gaaaaggcaa gacctaaact 120
 ggaacctgga agttaagcag aaccagggtg tggggagaga ggaacacatc actcaagatg 180
 gcacagcctg agcggccagg caaatatttc atatgaatgt ggccctgggt tggtagacact 240
 atgagcaaca tcagatttgg ggaagcaatt aaaaaaaaaa aaaaaattcc acaaaatggt 300
 ttacagacga tcttgcctat acagctggcc taaaaagcta ggcttagatt tttaaaatct 360
 cattttctga aaagagttgt tatacctcag tgttgtggcg agaggaataa aagcctcccc 420
 gcctcattca tgaggaactt cttagaagca catgctctgg gcaacatgcc ccgctagtct 480
 gagatttctc ctaatgctgc cagaaaccaa cctagtacac gtctctggtc ttccccaaca 540
 tctcccacgt tcaagctgct accttcagta ccatttctcc ccattcttcta cctttgagat 600
 atctacctgc aaggactaaa cagg 624

<210> 373
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 373

Met Leu Trp Ala Thr Cys Pro Ala Ser Leu Arg Phe Leu Leu Met Leu
 1 5 10 15

Pro Glu Thr Asn Leu Val His Val Ser Gly Leu Pro Gln His Leu Pro

20

25

30

Arg Ser Ser Cys Tyr Leu Gln Tyr His Phe Ser Pro Ser Ser Thr Phe
 35 40 45

Glu Ile Ser Thr Cys Lys Asp
 50 55

<210> 374
 <211> 440
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (162)..(162)
 <223> n = unknown

<400> 374
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 taggaggtac tagtgagaaa tatattttac agtctacata tntattgtat aataagctat 180
 attatattct aataacagca aatataacat tataatgatt ttgatatctg gactcgctag 240
 acttggtccc ataaatccta tagttcttaa caaaaaaacc catccgtag caaacttaca 300
 catctaagct cagtttaatg caacttaatg agacattgaa ttttatgcag ctaacccaag 360
 ttatctatag tgtgtgccct cctgagtacc ccaggaaata gaagtaaaga actgacgaac 420
 atcagatcca actggcccat 440

<210> 375
 <211> 30
 <212> PRT
 <213> Homo sapiens

<400> 375

Met Ile Leu Ile Ser Gly Leu Ala Arg Leu Gly Pro Ile Asn Pro Ile
 1 5 10 15

Val Leu Asn Lys Lys Thr His Pro Leu Ala Asn Leu His Ile
 20 25 30

<210> 376

<211> 348
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (315)..(315)
 <223> n = unknown

<400> 376
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 caaagacttt ccctgaaact ttgcgtggca tgggggttgc agaaactggt gtctacacat 180
 tacaaaagtg tactgtttac acctatttgt gatgcacca tcgtgttttt ctccatggac 240
 cacctattaa gcttctgct ggagcgctct tggccccctt cctgctttct gggccacatc 300
 ctgttgtaaa tcggngctac ttgtgggggtt ttgtttgtga attgggga 348

<210> 377
 <211> 32
 <212> PRT
 <213> Homo sapiens

<400> 377

Phe Phe Phe Phe Leu Gly Gln Gly Ile Leu Leu Arg Thr Leu Ser Leu
 1 5 10 15

Arg Lys Glu Ala Tyr Asn Ser Gly Lys Pro Phe Phe Phe Lys Asn Cys
 20 25 30

<210> 378
 <211> 2629
 <212> DNA
 <213> Homo sapiens

<400> 378
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 acatttcatt cgttaaagga ctatgtgtca gtaaggaaga ggataatcac tattcaatat 180
 caaaagatgc ctatatttct cgatgaggag gagcaacggc atctgcaggc actggaaaga 240
 gaagcagaag agcttttcca acaactacaa gacagtcaag tgagaatgac ccaacattta 300
 gaaaggatga aagacatgta cagagagctg tgggagacat gccacatgcc tgacgtggtg 360

ctgctccagg atgtgagaaa tgtatcagca aggactgatt tggcacagat gcaaaagccc	420
cagccagtga acccagagct cacttcacgg tgcataactg gagtcctaga catgctcaac	480
aacttcagag tggatagtgc tctgagcacg gaaatgattc cttgctatat aagcctttct	540
gaggatgtga gatagtgtat atttggagat gaccatctca gtgctcccac ggatccccag	600
ggagtggaca gctttgctgt gtggggagcg caagcattca cctccggcaa gcattactgg	660
gaggtggatg tgaccctctc ctccaactgg attctgggag tctgtcaaga ttccaggact	720
gcagatgcc aatttcgttat tgattctgat gaaagatttt ttttaatttc ctcaaagagg	780
agcaatcact atagtctctc caccaactct ccacctttaa ttcagtatgt gcaaaggcct	840
ctgggtcggg ttgggtgtgt tctggattat gataatggat ctgtgagttt ttttgatgtt	900
tctaaagggt ctcttatcta tggttttcct ccttcctcct tctcgtcccc tctgaggcct	960
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tatataaggc aaatactgtc ctaagacact atgtgtgaga gcctgtgagc gcactgtaac	1080
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tggtcttttt tgtacaagtt ttttgagatt cattcactta ctgtgaaagt catgtttctaa	1260
tgtattttaat tcagagattg ttagtatatc acacttgagc agccatcaga gctctcttct	1320
gcctgggcac ttttatcact tccagaagaa tcccaatacc ccttaacatt tattctgcat	1380
tcaccctccc ccattccttc agaacactta atctactttt tatgtttttg cattcgggta	1440
aataaaatca tacaacataa gttctttttt taatctgatt tatttttcag agagtatgtt	1500
ttcagtttgt gcacactgta aaccatttgt cttacttgta tatttgaacc aggctggggt	1560
agaaaaatga actggtggat atctcatctt acaaagaata aagaagtgtg cttattttct	1620
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cagattgaaa agtccaaggg ggcaatggca gtatttgtct tctttgctaa tatattacca	1860
ttatcgaatg cgatttttag aatagattac acaataaata agatgaataa atggattaag	1920
tagaggagtt agtatgtata aatattattc taacattgag aaacttttcc aaaatgtacg	1980
taacaaaata ggatagaaca tactaatgaa tatctatcaa aagataagac ataaattgat	2040

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tttcagattg atatcaaaga taatactatt atgttagggt ttaaaataat tgtagcataa 2100
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aatggcgtga acctgggagg cggggcttgc agtgagccaa gattgtgcca ctgcaatccg 2580
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<210> 379
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 379

Met Asp Tyr Leu Trp Glu Ile Asn Gln Glu Thr Arg Asn Asn Leu Asn
1 5 10 15

Gln Glu Thr Ser Thr Phe His Ser Leu Lys Asp Tyr Val Ser Val Arg
20 25 30

Lys Arg Ile Ile Thr Ile Gln Tyr Gln Lys Met Pro Ile Phe Leu Asp
35 40 45

Glu Glu Glu Gln Arg His Leu Gln Ala Leu Glu Arg Glu Ala Glu Glu
50 55 60

Leu Phe Gln Gln Leu Gln Asp Ser Gln Val Arg Met Thr Gln His Leu
65 70 75 80

Glu Arg Met Lys Asp Met Tyr Arg Glu Leu Trp Glu Thr Cys His Met
85 90 95

Pro Asp Val Val Leu Leu Gln Asp Val Arg Asn Val Ser Ala Arg Thr
100 105 110

Asp Leu Ala Gln Met Gln Lys Pro Gln Pro Val Asn Pro Glu Leu Thr
 115 120 125
 Ser Trp Cys Ile Thr Gly Val Leu Asp Met Leu Asn Asn Phe Arg Val
 130 135 140
 Asp Ser Ala Leu Ser Thr Glu Met Ile Pro Cys Tyr Ile Ser Leu Ser
 145 150 155 160
 Glu Asp Val Arg Tyr Val Ile Phe Gly Asp Asp His Leu Ser Ala Pro
 165 170 175
 Thr Asp Pro Gln Gly Val Asp Ser Phe Ala Val Trp Gly Ala Gln Ala
 180 185 190
 Phe Thr Ser Gly Lys His Tyr Trp Glu Val Asp Val Thr Leu Ser Ser
 195 200 205
 Asn Trp Ile Leu Gly Val Cys Gln Asp Ser Arg Thr Ala Asp Ala Asn
 210 215 220
 Phe Val Ile Asp Ser Asp Glu Arg Phe Phe Leu Ile Ser Ser Lys Arg
 225 230 235 240
 Ser Asn His Tyr Ser Leu Ser Thr Asn Ser Pro Pro Leu Ile Gln Tyr
 245 250 255
 Val Gln Arg Pro Leu Gly Arg Val Gly Val Phe Leu Asp Tyr Asp Asn
 260 265 270
 Gly Ser Val Ser Phe Phe Asp Val Ser Lys Gly Ser Leu Ile Tyr Gly
 275 280 285
 Phe Pro Pro Ser Ser Phe Ser Ser Pro Leu Arg Pro Phe Phe Cys Phe
 290 295 300
 Gly Cys Thr
 305

<210> 380
 <211> 720
 <212> DNA
 <213> Homo sapiens

<400> 380
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 tcatacggtc ccttagacat gtaccggaac ccggggccct cggggcccca gctccgggac 120
 ttcagcagca tcatccagac gtgcagcggc aacatccagc ggatcagcca agccactgct 180
 cagataaaga atttgatgag ccagctagga actaagcagg actcaagcaa gctacaggaa 240
 aatctgcaac agttacaaca ctccacaaat cagctcgcca aggaaacaaa tgaattgctg 300
 aaagaattag ggtccttgcc ccttccctta tctacttcag aacagcgcca gcagagactt 360
 cagacggcac gcctcatgaa tgacttctct gcagccttaa acaatttcca ggctgtgcag 420
 agcaagggtta tctgacacag gacacaggcg agtattgcca cgagccaaga gctggcatct 480
 ccgtctctcc tgcccgacag agcaggcccc agagcaggag ccagctgcgt ctgattccga 540
 ccagcccatg cagcgagtcg ccaccacga tgcccgacc cagggcaggc atccaccgcy 600
 cgccatcacc tgcacccccg caccgcgcgc cacctccact ccaccccaac ccgacccaac 660
 cccggcacac ccccgcccac cctgccaggc ctgcgcccc ccccgcccc tccccaccc 720

<210> 381
 <211> 1175
 <212> DNA
 <213> Homo sapiens

<400> 381
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 tctaaaggca atttaaaaat catgtcaagc tcagttgaac agaaaaaagg gcctacaaga 180
 cagcgcaaat gtggcttttg taagtcaaat agagacaagg aatgtggaca gttactaata 240
 tctgaaaacc agaaggtggc agcgcacat aagtgcagtc tcttttcac tgctttggta 300
 tcatcacact ctgataatga aagtcttggg ggattttcta ttgaagatgt ccaaaggaa 360
 attaaaagag gcacgaagct gatgtgttct ttgtgccatt gtcttgagc aacaattggg 420
 tgtgatgtga aaacatgtca caggacatac cactaccact gtgcattgca tgataaagct 480
 caaatacgag agaaaccttc acaaggaatt tacatggcct attgccgaaa acacaagaaa 540
 actgcacata actccgaagc agctgattta gaagaaagtt ttaatgaaca tgaactggag 600
 ccctcatcac ctaaaagtaa aaagaaaagt cgcaaaggaa ggccaagaaa aactaatatt 660
 aaagggctgt cagaagatac caggtccaca tcctcccatg gaacagatga aatggaaagt 720

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agttcctata gagataggtc tccacacaga agcagcccta gtgacaccag gcctaaatgt      780
ggattttgcc atgtagggga ggaagaaaat 'gaagcacgag gaaaactgca tatattttaat      840
gccagaagg cagctgcca ttataagtgc atgttgtttt cttctggcac agtccagctc      900
acaacaacat caagagcaga atttgagac tttgatatta aaactgtact tcaggagatt      960
aaacgaggaa aaagaatggt ctgtagtttt tatatttggt atgcaacatt acacttgatt     1020
tgctgcttta aatttagagt acatcccaaa tttatccagt catcagaaaa tttaaagtag     1080
ttcgtatggt aaagcaaagt atatatttga cttatttgta atataataaa ggatgctgat     1140
gttacgga   aaaaaaaaaa aaaaaaaaaa aaaaaa                                1175

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<210> 382
<211> 125
<212> PRT
<213> Homo sapiens

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<400> 382

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Met Ser Tyr Gly Pro Leu Asp Met Tyr Arg Asn Pro Gly Pro Ser Gly
1          5          10          15

```

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Pro Gln Leu Arg Asp Phe Ser Ser Ile Ile Gln Thr Cys Ser Gly Asn
          20          25          30

```

```

Ile Gln Arg Ile Ser Gln Ala Thr Ala Gln Ile Lys Asn Leu Met Ser
          35          40          45

```

```

Gln Leu Gly Thr Lys Gln Asp Ser Ser Lys Leu Gln Glu Asn Leu Gln
          50          55          60

```

```

Gln Leu Gln His Ser Thr Asn Gln Leu Ala Lys Glu Thr Asn Glu Leu
          65          70          75          80

```

```

Leu Lys Glu Leu Gly Ser Leu Pro Leu Pro Leu Ser Thr Ser Glu Gln
          85          90          95

```

```

Arg Gln Gln Arg Leu Gln Thr Ala Arg Leu Met Asn Asp Phe Ser Ala
          100          105          110

```

```

Ala Leu Asn Asn Phe Gln Ala Val Gln Ser Lys Gly Ile
          115          120          125

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<210> 383
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 383

Met Ser Ser Ser Val Glu Gln Lys Lys Gly Pro Thr Arg Gln Arg Lys
 1 5 10 15

Cys Gly Phe Cys Lys Ser Asn Arg Asp Lys Glu Cys Gly Gln Leu Leu
 20 25 30

Ile Ser Glu Asn Gln Lys Val Ala Ala His His Lys Cys Met Leu Phe
 35 40 45

Ser Ser Ala Leu Val Ser Ser His Ser Asp Asn Glu Ser Leu Gly Gly
 50 55 60

Phe Ser Ile Glu Asp Val Gln Lys Glu Ile Lys Arg Gly Thr Lys Leu
 65 70 75 80

Met Cys Ser Leu Cys His Cys Pro Gly Ala Thr Ile Gly Cys Asp Val
 85 90 95

Lys Thr Cys His Arg Thr Tyr His Tyr His Cys Ala Leu His Asp Lys
 100 105 110

Ala Gln Ile Arg Glu Lys Pro Ser Gln Gly Ile Tyr Met Ala Tyr Cys
 115 120 125

Arg Lys His Lys Lys Thr Ala His Asn Ser Glu Ala Ala Asp Leu Glu
 130 135 140

Glu Ser Phe Asn Glu His Glu Leu Glu Pro Ser Ser Pro Lys Ser Lys
 145 150 155 160

Lys Lys Ser Arg Lys Gly Arg Pro Arg Lys Thr Asn Phe Lys Gly Leu
 165 170 175

Ser Glu Asp Thr Arg Ser Thr Ser Ser His Gly Thr Asp Glu Met Glu
 180 185 190

Ser Ser Ser Tyr Arg Asp Arg Ser Pro His Arg Ser Ser Pro Ser Asp

195 200 205

Thr Arg Pro Lys Cys Gly Phe Cys His Val Gly Glu Glu Glu Asn Glu
210 215 220

Ala Arg Gly Lys Leu His Ile Phe Asn Ala Lys Lys Ala Ala Ala His
225 230 235 240

Tyr Lys Cys Met Leu Phe Ser Ser Gly Thr Val Gln Leu Thr Thr Thr
245 250 255

Ser Arg Ala Glu Phe Gly Asp Phe Asp Ile Lys Thr Val Leu Gln Glu
260 265 270

Ile Lys Arg Gly Lys Arg Met Val Cys Ser Phe Tyr Ile Cys Tyr Ala
275 280 285

Thr Leu His Leu Ile Cys Cys Phe Lys Phe Arg Val His Pro Lys Phe
290 295 300

Ile Gln Ser Ser Glu Asn Leu Lys
305 310

<210> 384
<211> 589
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(589)
<223> n = unknown

<400> 384
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actttggaga gaaactggcc atgacgtatg gggcattatt ctgtgaaaca agtgccaaag 180
atggttctaa catagtggag gctgttctgc accttgctcg agaagtgaaa aagagaactg 240
acaaggatga cagcagatcc attaccaatc taaccgggac caattccaaa aagtcaccac 300
agatgaagaa ttgttgcaat ggctaaatcc caaacatcct tggcctgtga agtcttcatt 360
tccagaatac tgaatttgtg tgacttattt gggctttaac agagtgggca catcctactg 420

acactgtcct tggggagttt acagtgcagg ganacctgaa cccggttctc aggtncctct 480
 ggaacttttg gtcttctttg ttttgtctca gtgagtgnntt gggcctctgn taaataggtg 540
 gtctgtctta caggtnntaa aggttanctg taatgttttt aaatggtaa 589

<210> 385
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 385

Met Ile Glu Asp Ala Ala His Glu Thr Val Pro Ile Met Leu Val Gly
 1 5 10 15

Asn Lys Ala Asp Ile Arg Asp Thr Ala Ala Thr Glu Gly Gln Lys Cys
 20 25 30

Val Pro Gly His Phe Gly Glu Lys Leu Ala Met Thr Tyr Gly Ala Leu
 35 40 45

Phe Cys Glu Thr Ser Ala Lys Asp Gly Ser Asn Ile Val Glu Ala Val
 50 55 60

Leu His Leu Ala Arg Glu Val Lys Lys Arg Thr Asp Lys Asp Asp Ser
 65 70 75 80

Arg Ser Ile Thr Asn Leu Thr Gly Thr Asn Ser Lys Lys Ser Pro Gln
 85 90 95

Met Lys Asn Cys Cys Asn Gly
 100

<210> 386
 <211> 1101
 <212> DNA
 <213> Homo sapiens

<400> 386

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 ctggtgcccc tggagaagcc agtgaccctc cgggtgccagg gacctccggg cgtggacctg 180
 taccgcttg agaagctgag ttccagcagg taccaggatc aggcagtcct cttcatcccg 240


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gccatgaaga gaagtctggc tggacgctac cgctgctcct accagaacgg aagcctctgg 300
tccctgcca gcgaccagct ggagctcggt gccacgggag tttttgcaa accctcgctc 360
tcagcccagc cgggcccggc ggtgtcgtca ggaggggacg taacctaca gtgtcagact 420
cggatatggct ttgaccaatt tgctctgtac aaggaagggg accctgcgcc ctacaagaat 480
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<210> 387
<211> 339
<212> PRT
<213> Homo sapiens

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<400> 387

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Met Ser Pro Ser Pro Thr Ala Leu Phe Cys Leu Gly Leu Cys Leu Gly
1           5           10           15

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```

Arg Val Pro Ala Gln Ser Gly Pro Leu Pro Lys Pro Ser Leu Gln Ala
          20           25           30

```

```

Leu Pro Ser Ser Leu Val Pro Leu Glu Lys Pro Val Thr Leu Arg Cys
          35           40           45

```

```

Gln Gly Pro Pro Gly Val Asp Leu Tyr Arg Leu Glu Lys Leu Ser Ser
          50           55           60

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```

Ser Arg Tyr Gln Asp Gln Ala Val Leu Phe Ile Pro Ala Met Lys Arg
65           70           75           80

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Ser Leu Ala Gly Arg Tyr Arg Cys Ser Tyr Gln Asn Gly Ser Leu Trp
 85 90 95

Ser Leu Pro Ser Asp Gln Leu Glu Leu Val Ala Thr Gly Val Phe Ala
 100 105 110

Lys Pro Ser Leu Ser Ala Gln Pro Gly Pro Ala Val Ser Ser Gly Gly
 115 120 125

Asp Val Thr Leu Gln Cys Gln Thr Arg Tyr Gly Phe Asp Gln Phe Ala
 130 135 140

Leu Tyr Lys Glu Gly Asp Pro Ala Pro Tyr Lys Asn Pro Glu Arg Trp
 145 150 155 160

Tyr Arg Ala Ser Phe Pro Ile Ile Thr Val Thr Ala Ala His Ser Gly
 165 170 175

Thr Tyr Arg Cys Tyr Ser Phe Ser Ser Arg Asp Pro Tyr Leu Trp Ser
 180 185 190

Ala Pro Ser Asp Pro Leu Glu Leu Val Val Thr Gly Thr Ser Val Thr
 195 200 205

Pro Ser Arg Leu Pro Thr Glu Pro Pro Ser Ser Val Ala Glu Phe Ser
 210 215 220

Glu Ala Thr Ala Glu Leu Thr Val Ser Phe Thr Asn Lys Val Phe Thr
 225 230 235 240

Thr Glu Thr Ser Arg Ser Ile Thr Thr Ser Pro Lys Glu Ser Asp Ser
 245 250 255

Pro Ala Gly Pro Ala Arg Gln Tyr Tyr Thr Lys Gly Asn Leu Val Arg
 260 265 270

Ile Cys Leu Gly Ala Val Ile Leu Ile Ile Leu Ala Gly Phe Leu Ala
 275 280 285

Glu Asp Trp His Ser Arg Arg Lys Arg Leu Arg His Arg Gly Arg Ala
 290 295 300

Val Gln Arg Pro Leu Pro Pro Leu Pro Pro Leu Pro Gln Thr Arg Lys
 305 310 315 320

Ser His Gly Gly Gln Asp Gly Gly Arg Gln Asp Val His Ser Arg Gly
 325 330 335

Leu Cys Ser

<210> 388

<211> 1226

<212> DNA

<213> Homo sapiens

<400> 388

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agccggaagc agcagaacgt ggaccgggcc atggccaagc tgcaggggga ggggctgagt      240
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gacatccggg taaactgcgt ggttccagga attatcaaaa ctgacttcag caaagtgttt      660
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tttatcctca aaaaaaaaaa aaaaaa 1226

<210> 389

<211> 258

<212> PRT

<213> Homo sapiens

<400> 389

Met Ser Ser Thr Gly Ile Asp Arg Lys Gly Val Leu Ala Asn Arg Val
1 5 10 15

Ala Val Val Thr Gly Ser Thr Ser Gly Ile Gly Phe Ala Ile Ala Arg
20 25 30

Arg Leu Ala Arg Asp Gly Ala His Val Val Ile Ser Ser Arg Lys Gln
35 40 45

Gln Asn Val Asp Arg Ala Met Ala Lys Leu Gln Gly Glu Gly Leu Ser
50 55 60

Val Ala Gly Ile Val Cys His Val Gly Lys Ala Glu Asp Arg Glu Gln
65 70 75 80

Leu Val Ala Lys Ala Leu Glu His Cys Gly Gly Val Asp Phe Leu Val
85 90 95

Cys Ser Ala Gly Val Asn Pro Leu Val Gly Ser Thr Leu Gly Thr Ser
100 105 110

Glu Gln Ile Trp Asp Lys Ile Leu Ser Val Asn Val Lys Ser Pro Ala
115 120 125

Leu Leu Leu Ser Gln Leu Leu Pro Tyr Met Glu Asn Arg Arg Gly Ala
130 135 140

Val Ile Leu Val Ser Ser Ile Ala Ala Tyr Asn Pro Val Val Ala Leu
145 150 155 160

Gly Val Tyr Asn Val Ser Lys Thr Ala Leu Leu Gly Leu Thr Arg Thr
165 170 175

Leu Ala Leu Glu Leu Ala Pro Lys Asp Ile Arg Val Asn Cys Val Val
 180 185 190

Pro Gly Ile Ile Lys Thr Asp Phe Ser Lys Val Phe His Gly Asn Glu
 195 200 205

Ser Leu Trp Lys Asn Phe Lys Glu His His Gln Leu Gln Arg Ile Gly
 210 215 220

Glu Ser Glu Asp Cys Ala Gly Ile Val Ser Phe Leu Cys Ser Pro Asp
 225 230 235 240

Ala Ser Tyr Val Asn Gly Glu Asn Ile Ala Val Ala Gly Tyr Ser Thr
 245 250 255

Arg Leu

<210> 390
 <211> 605
 <212> DNA
 <213> Homo sapiens

<400> 390
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 gctttttccag tccagagagg ccacccccac ccaacttgag aaaagaaaa tagctcagat 180
 cagtctgagc tatgcgaaat gtatcaggcc caggagagact gtacagtga taggggactt 240
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 aaaaa 605

<210> 391
 <211> 63
 <212> PRT

<213> Homo sapiens

<400> 391

Met Lys Ser His Tyr Ile Val Gln Ala Gly Leu Lys Leu Leu Ala Ser
1 5 10 15

Ser Asp Pro Pro Pro Thr Ser Ala Ser His Ser Ala Gly Ile Ile Gly
20 25 30

Met Ser Gln Arg Thr Gln Ser Ala Ser Gly Phe Leu Arg Asn Lys Glu
35 40 45

Glu Arg Val Pro Lys Leu Leu Pro Arg Ile Tyr Ile Glu Thr Ala
50 55 60

<210> 392

<211> 297

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (219)..(294)

<223> n = unknown

<400> 392

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tcccccggtg aatgaggggt ttctgttgtt aatggggggg gggaccggcc cccctctgct 180
ttgcgccacc cttaaaaggg actttaggcc ctagaccana accttgcccc ccccccccaa 240
gaaacgttcc ttcatacaaga aaacgggggt ccccccccca aaaccccccc cctntcg 297

<210> 393

<211> 51

<212> PRT

<213> Homo sapiens

<400> 393

Met Met Ser Gly Leu Arg Asp Arg Arg Lys Met Gly Asp Arg Gly Phe
1 5 10 15

Thr Leu Arg Gly Phe Pro Pro Val Asn Glu Gly Phe Leu Leu Leu Met
20 25 30

Gly Gly Gly Thr Gly Pro Pro Leu Leu Cys Ala Thr Leu Lys Arg Asp
 35 40 45

Phe Arg Pro
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<210> 394
 <211> 263
 <212> DNA
 <213> Homo sapiens

<400> 394
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 cataagctgc cttttgtga ggcccttcag ctaactattt ctccactgca gcagtagatc 180
 agttcagaag aaaactgtac attcccagca agaatgccaa cagaaacaaa tggttgctat 240
 ttaaaataaa tagtggttaa acg 263

<210> 395
 <211> 738
 <212> DNA
 <213> Homo sapiens

<400> 395
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 tgctaaaaac attgaccata caagcaaaga ttaaattagc ctatattaat cataataact 180
 gtttatcgca catgtacccc ttaacctaaa agatgaagaa gaaaataaaa aataaaataa 240
 aatttgaaga aaatgttaaa caaaaatgaa accataccag tactagaaga aaaatgggtg 300
 aattcctctt taacctaggc aaaggaaagg cttctctggc tccaatctg gatttaatta 360
 atcctaaagt tgtatagaat cacaaaatac ctcaaatagc caaaacaatc ctgagcaaag 420
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 tctttaggaa aaggatagtc tctttaaaaa atggtgctgt gtaaactaga tatccgtatg 660
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atgtagaccc aaatgcaa

738

<210> 396

<211> 2430

<212> DNA

<213> Homo sapiens

<400> 396

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 tctctgacct acaaaaaaaaa aaaaaaaaaa 2430

<210> 397
 <211> 730
 <212> PRT
 <213> Homo sapiens

<400> 397

Met Gly Val Cys Gln Arg Thr Arg Ala Pro Trp Lys Glu Lys Ser Gln
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Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Gly Ser Gly Met Phe
 20 25 30

Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala Gly Ser Met
 35 40 45

Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu Pro Leu Leu Leu
 50 55 60

Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp Leu Pro Ala Asp Leu
 65 70 75 80
 Ala Phe Ala Val Arg Ala Leu Cys Cys Lys Arg Ala Leu Arg Ala Arg
 85 90 95
 Ala Leu Ala Ala Ala Ala Asp Pro Glu Gly Pro Glu Gly Gly Cys
 100 105 110
 Ser Leu Ala Trp Arg Leu Ala Glu Leu Ala Gln Gln Arg Ala Ala His
 115 120 125
 Thr Phe Leu Ile His Gly Ser Arg Arg Phe Ser Tyr Ser Glu Ala Glu
 130 135 140
 Arg Glu Ser Asn Arg Ala Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp
 145 150 155 160
 Asp Trp Gly Pro Asp Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu
 165 170 175
 Gly Glu Arg Ala Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly
 180 185 190
 Ala Glu Phe Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala
 195 200 205
 Ala Pro Leu Ser Pro Gly Ala Thr Val Ala Leu Leu Leu Pro Ala Gly
 210 215 220
 Pro Glu Phe Leu Trp Leu Trp Phe Gly Leu Ala Lys Ala Gly Leu Arg
 225 230 235 240
 Thr Ala Phe Val Pro Thr Ala Leu Arg Arg Gly Pro Leu Leu His Cys
 245 250 255
 Leu Arg Ser Cys Gly Ala Arg Ala Leu Val Leu Ala Pro Glu Phe Leu
 260 265 270
 Glu Ser Leu Glu Pro Asp Leu Pro Ala Leu Arg Ala Met Gly Leu His
 275 280 285

Leu Trp Ala Ala Gly Pro Gly Thr His Pro Ala Gly Ile Ser Asp Leu
 290 295 300

Leu Ala Glu Val Ser Ala Glu Val Asp Gly Pro Val Pro Gly Tyr Leu
 305 310 315 320

Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys Leu Tyr Ile Phe Thr Ser
 325 330 335

Gly Thr Thr Gly Leu Pro Lys Ala Ala Arg Ile Ser His Leu Lys Ile
 340 345 350

Leu Gln Cys Gln Gly Phe Tyr Gln Leu Cys Gly Val His Gln Glu Asp
 355 360 365

Val Ile Tyr Leu Ala Leu Pro Leu Tyr His Met Ser Gly Ser Leu Leu
 370 375 380

Gly Ile Val Gly Cys Met Gly Ile Gly Ala Thr Val Val Leu Lys Ser
 385 390 395 400

Lys Phe Ser Ala Gly Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val
 405 410 415

Thr Val Phe Gln Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln
 420 425 430

Pro Pro Ser Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly
 435 440 445

Ser Gly Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly
 450 455 460

Pro Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala
 465 470 475 480

Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser Trp
 485 490 495

Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp Val Thr
 500 505 510

Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met Ala Thr Ser
 515 520 525

Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser Gln Gln Ser Pro
 530 535 540

Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala Gln Gly Lys Leu Leu
 545 550 555 560

Lys Asp Val Phe Arg Pro Gly Asp Val Phe Phe Asn Thr Gly Asp Leu
 565 570 575

Leu Val Cys Asp Asp Gln Gly Phe Leu Arg Phe His Asp Arg Thr Gly
 580 585 590

Asp Thr Phe Arg Trp Lys Gly Glu Asn Val Ala Thr Thr Glu Val Ala
 595 600 605

Glu Val Phe Glu Ala Leu Asp Phe Leu Gln Glu Val Asn Val Tyr Gly
 610 615 620

Val Thr Val Pro Gly His Glu Gly Arg Ala Gly Met Ala Ala Leu Val
 625 630 635 640

Leu Arg Pro Pro His Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val
 645 650 655

Ser Glu Asn Leu Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln
 660 665 670

Glu Ser Leu Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met
 675 680 685

Ala Asn Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val
 690 695 700

Leu Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr
 705 710 715 720

Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile
 725 730

<210> 398
 <211> 3274
 <212> DNA
 <213> Homo sapiens

<400> 398
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 aactgggcca agcggctgcc gctttccgcg tggagcgcac tgactaccgc agctcccacg 240
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<210> 399

<211> 162

<212> PRT

<213> Homo sapiens

<400> 399

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20 25 30

Asp Arg Ser Leu Glu Asp Gly Leu Asn Arg Glu Leu Arg Glu Glu Leu
35 40 45

Gly Glu Ala Ala Ala Ala Phe Arg Val Glu Arg Thr Asp Tyr Arg Ser
50 55 60

Ser His Val Gly Ser Gly Pro Arg Val Val Ala His Phe Tyr Ala Lys
65 70 75 80

Arg Leu Thr Leu Glu Glu Leu Leu Ala Val Glu Ala Gly Ala Thr Arg
85 90 95

Ala Lys Asp His Gly Leu Glu Val Leu Gly Leu Val Arg Val Pro Leu
100 105 110

Tyr Thr Leu Arg Asp Gly Val Gly Gly Leu Pro Thr Phe Leu Glu Asn
115 120 125

Ser Phe Ile Gly Ser Ala Arg Glu Gln Leu Leu Glu Ala Leu Gln Asp
130 135 140

Leu Gly Leu Leu Gln Ser Gly Ser Ile Ser Gly Leu Lys Ile Pro Ala
145 150 155 160

His His

<210> 400
 <211> 2480
 <212> DNA
 <213> Homo sapiens

<400> 400
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<210> 401
<211> 320
<212> PRT
<213> Homo sapiens
<400> 401

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Met Glu Leu Leu Ser Pro Pro Leu Arg Asp Val Asp Leu Thr Ala Pro
1          5          10          15

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Asp Gly Ser Leu Cys Ser Phe Ala Thr Thr Asp Asp Phe Tyr Asp Asp
          20          25          30

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Pro Cys Phe Asp Ser Pro Asp Leu Arg Phe Phe Glu Asp Leu Asp Pro
          35          40          45

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Arg Leu Met His Val Gly Ala Leu Leu Lys Pro Glu Glu His Ser His
50          55          60

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Phe Pro Ala Ala Val His Pro Ala Pro Gly Ala Arg Glu Asp Glu His
 65 70 75 80
 Val Arg Ala Pro Ser Gly His His Gln Ala Gly Arg Cys Leu Leu Trp
 85 90 95
 Ala Cys Lys Ala Cys Lys Arg Lys Thr Thr Asn Ala Asp Arg Arg Lys
 100 105 110
 Ala Ala Thr Met Arg Glu Arg Arg Arg Leu Ser Lys Val Asn Glu Ala
 115 120 125
 Phe Glu Thr Leu Lys Arg Cys Thr Ser Ser Asn Pro Asn Gln Arg Leu
 130 135 140
 Pro Lys Val Glu Ile Leu Arg Asn Ala Ile Arg Tyr Ile Glu Gly Leu
 145 150 155 160
 Gln Ala Leu Leu Arg Asp Gln Asp Ala Ala Pro Pro Gly Ala Ala Ala
 165 170 175
 Ala Phe Tyr Ala Pro Gly Pro Leu Pro Pro Gly Arg Gly Gly Glu His
 180 185 190
 Tyr Ser Gly Asp Ser Asp Ala Ser Ser Pro Arg Ser Asn Cys Ser Asp
 195 200 205
 Gly Met Met Asp Tyr Ser Gly Pro Pro Ser Gly Ala Arg Arg Arg Asn
 210 215 220
 Cys Tyr Glu Gly Ala Tyr Tyr Asn Glu Ala Pro Ser Glu Pro Arg Pro
 225 230 235 240
 Gly Lys Ser Ala Ala Val Ser Ser Leu Asp Cys Leu Ser Ser Ile Val
 245 250 255
 Glu Arg Ile Ser Thr Glu Ser Pro Ala Ala Pro Ala Leu Leu Leu Ala
 260 265 270
 Asp Val Pro Ser Glu Ser Pro Pro Arg Arg Gln Glu Ala Ala Ala Pro
 275 280 285

Ser Glu Gly Glu Ser Ser Gly Asp Pro Thr Gln Ser Pro Asp Ala Ala
 290 295 300

Pro Gln Cys Pro Ala Gly Ala Asn Pro Asn Pro Ile Tyr Gln Val Leu
 305 310 315 320

<210> 402

<211> 2290

<212> DNA

<213> Homo sapiens

<400> 402

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ctgtttttct ccttctctta ttccatttag tttttcaatt catacaaaac tgtatccagg      180
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aacactacca agtacaagcc ccggacactg gaccagagc aacccctggg catctgctct     1260

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<210> 403
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 403

Met Glu Glu Thr Asn Ser Ser Ser Lys Asp Met Tyr Gln Ser Pro Gly
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Glu Ala Glu Gly Trp Arg Trp Lys Lys Gly Ser Asp Arg Gly Gln Asn
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Leu Phe Arg Lys His Ser Lys Cys Leu Ile Leu Leu Ile Arg Glu Arg
 35 40 45

Phe Glu Ser Pro His Ser Tyr Ile Cys Ser Pro Val Thr Phe Gln Phe
 50 55 60
 Phe Tyr Ala Gln Ser Val Lys His Val Asn Val Thr Ile Asp Cys Leu
 65 70 75 80
 Pro Glu Gly Ala Ala Thr Arg Gly Thr Ala Arg Thr Ser Lys Pro Thr
 85 90 95
 Thr Lys Ser Gln Lys Thr Leu Pro Ser Thr Ser Pro Gly His Trp Thr
 100 105 110
 Gln Ser Thr Pro Trp Ala Ser Ala Leu Arg Ser Ser Pro Trp Thr Glu
 115 120 125
 Thr Ala Ala Pro Ser Glu Thr Glu Glu Thr Leu Asn Thr Gly Arg Pro
 130 135 140
 Pro Glu Leu Pro Ala Arg Ala Thr Ala Thr Trp Phe Ser Ala Ser His
 145 150 155 160
 Thr Leu Pro Ala Leu Ala Thr Arg Arg Val Ala Arg Thr Gln Trp Leu
 165 170 175
 Thr Ala Asp Arg Gln Thr Trp Ala Ser Ile Ser Ser Val Pro Trp Ala
 180 185 190
 Gln Thr Ile Ser Glu Lys Lys Pro Gly Gly Ser Leu Trp Glu Thr Arg
 195 200 205
 Ser Ser Pro Pro Thr Thr Ala Gly Thr Glu Glu Ala Met Asn Thr Thr
 210 215 220
 Ser Leu Leu Ala Pro Ala Ala Glu Ile Met Ala Thr Pro Gly Ser Pro
 225 230 235 240
 Ser Gln Ala Ser Pro Thr Ser Gly Ala Phe Thr His Gly Thr Gln Thr
 245 250 255
 Pro Ser Pro Thr Lys Ala Thr Ala Pro Arg Tyr Pro Gln Thr Gly Asp
 260 265 270

Leu Ser Ala Glu Trp Pro Phe Thr Ala Gly Glu Glu Pro Val Leu Val
 275 280 285

Pro Arg Pro His Gln Val Ser Arg Cys Pro Gln Pro Leu Phe Lys Val
 290 295 300

Gly Ala Met Ala Ala Ala Pro Leu Thr Leu Ala Ile Gln Arg Leu Asn
 305 310 315 320

Pro Cys Leu Met Glu Leu Cys Gln Phe Phe Gln Gln Cys Leu Cys Met
 325 330 335

Ser Gln Arg Ser Pro Arg Thr Glu Asp Met Arg Tyr Cys Leu Glu Tyr
 340 345 350

Tyr Ser Trp Phe Leu Lys Asn Ala Thr Tyr Ile Cys Gln Arg Val Lys
 355 360 365

Arg Val Ser His Ser His Thr Leu Lys Gln Lys Cys Leu Glu Asn Ile
 370 375 380

Cys Lys Ser Val
 385

<210> 404
 <211> 546
 <212> DNA
 <213> Homo sapiens

<400> 404
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 tcctacagaa aatgcagcat ccctggtgat agcagaagag ctgttacttt tagtgacatt 480
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caacct

546

<210> 405
 <211> 21
 <212> PRT
 <213> Homo sapiens

<400> 405

Met Cys His His Phe Leu Ile Lys Ile Arg Asp Leu Ile Leu Gln Lys
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Met Gln His Pro Trp
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<210> 406
 <211> 546
 <212> DNA
 <213> Homo sapiens

<400> 406

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<210> 407
 <211> 21
 <212> PRT
 <213> Homo sapiens

<400> 407

Met Cys His His Phe Leu Ile Lys Ile Arg Asp Leu Ile Leu Gln Lys
 1 5 10 15

Met Gln His Pro Trp
20

<210> 408
<211> 1977
<212> DNA
<213> Homo sapiens

<400> 408
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 gccactgcac tccagcctgg gctacagagc gagactctac ctcaaaaaaa aaaaaaa 1977

<210> 409
 <211> 284
 <212> PRT
 <213> Homo sapiens

<400> 409

Met Val Glu Phe Ala Pro Leu Phe Met Pro Trp Glu Arg Arg Leu Gln
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Thr Leu Ala Val Leu Gln Phe Val Phe Ser Phe Leu Ala Leu Ala Glu
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Ile Cys Thr Val Gly Phe Ile Ala Leu Leu Phe Thr Arg Phe Trp Leu
35 40 45

Leu Thr Val Leu Tyr Ala Ala Trp Trp Tyr Leu Asp Arg Asp Lys Pro
50 55 60

Arg Gln Gly Gly Arg His Ile Gln Ala Ile Arg Cys Trp Thr Ile Trp
65 70 75 80

Lys Tyr Met Lys Asp Tyr Phe Pro Ile Ser Leu Val Lys Thr Ala Glu
85 90 95

Leu Asp Pro Ser Arg Asn Tyr Ile Ala Gly Phe His Pro His Gly Val
100 105 110

Leu Ala Val Gly Ala Phe Ala Asn Leu Cys Thr Glu Ser Thr Gly Phe
 115 120 125

Ser Ser Ile Phe Pro Gly Ile Arg Pro His Leu Met Met Pro Thr Leu
 130 135 140

Trp Phe Arg Ala Pro Phe Phe Arg Asp Tyr Ile Met Ser Ala Gly Leu
 145 150 155 160

Val Thr Ser Glu Lys Glu Ser Ala Ala His Ile Leu Asn Arg Lys Gly
 165 170 175

Gly Gly Asn Leu Leu Gly Ile Ile Val Gly Gly Ala Gln Glu Ala Leu
 180 185 190

Asp Ala Arg Pro Gly Ser Phe Thr Leu Leu Leu Arg Asn Arg Lys Gly
 195 200 205

Phe Val Arg Leu Ala Leu Thr His Gly Tyr Gln Ala Ser Gly Lys Ser
 210 215 220

Thr Leu Gly Ser Val Gly Asn Trp Gln Gly Phe Tyr Phe Gly Gly Lys
 225 230 235 240

Met Ala Glu Thr Asn Ala Asp Ser Ile Leu Val Glu Ile Phe Ser Pro
 245 250 255

Phe Thr Ile Lys Ile Ile Phe Trp Cys Leu Met Pro Lys Tyr Leu Glu
 260 265 270

Lys Phe Pro Gln Arg Arg Leu Ser Asp Leu Arg Asn
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<210> 410

<211> 1549

<212> DNA

<213> Homo sapiens

<400> 410

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agcgagttct tcaagaccta tatctgcctc ccgccggctc aactgtatca ctgggtggag 180

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caccgccggt ttacctgac agtggttaacc ttactggga cactcatctg ttacactgga      960
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<211> 179

<212> PRT

<213> Homo sapiens

<400> 411

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 35 40 45

Tyr His Trp Val Glu Met Arg Thr Lys Met Arg Ile Met Gly Phe Arg
 50 55 60

Gly Thr Val Ile Lys Pro Leu Asn Glu Glu Ala Ala Ala Glu Leu Gly
 65 70 75 80

Ala Glu Leu Leu Gly Glu Ala Thr Ile Phe Ile Val Gly Gly Gly Cys
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Leu Val Leu Glu Tyr Trp Arg His Gln Ala Gln Gln Arg His Lys Glu
 100 105 110

Glu Glu Gln Arg Ala Ala Trp Asn Ala Leu Arg Asp Glu Val Gly His
 115 120 125

Leu Ala Leu Ala Leu Glu Ala Leu Gln Ala Gln Val Gln Ala Ala Pro
 130 135 140

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Ser Lys Lys

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gccactacgc ccggctaatt ttttgtatit ttttagtaga gacgggggtt caccgtttta      180
gccgggatgg tctcgatctc ctgacctcgt gatccaccgc cctcggcctc ccaaaatgct      240
gggattacag gcgtgagcca ccgcgcccgg cctcttacat gtttttttta agcttttaaaa      300
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<400> 413

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Ala Leu Ser Pro Arg Leu Glu Cys Xaa Gly Ala Ile Ser Ala His Cys
1           5           10           15

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Lys Leu Arg Leu Pro Gly Ser Arg His Ser Pro Ala Ser Ala Ser Gln
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```

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Val Ala Gly Thr Thr Gly Ala Arg His Tyr Ala Arg Leu Ile Phe Cys
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Ile Phe Leu Val Glu Thr Gly Phe His Arg Phe Ser Arg Asp Gly Leu
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 <212> DNA
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<212> PRT

<213> Homo sapiens

<400> 415

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20          25          30

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```

Glu Gly Leu Arg Lys His Tyr Leu Leu Pro Ala Ile Glu Tyr Phe Asn
35          40          45

```

```

Gly Gly Pro Pro Ala Glu Thr Asp Phe Gly Gly Asp Tyr Gly Gly Thr
50          55          60

```

```

Gln Tyr Ser Leu Val Val Phe Asn Thr Val Asp Cys Ala Pro Glu Ser
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Tyr Val Gln Cys His Ala Pro Thr Ser Ser Ala Tyr Glu Phe Val Thr
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Trp Leu Asp Gly Ile Lys Phe Met Gly Gly Gly Gly Glu Ser Cys Ser
100 105 110

Leu Ile Ala Glu Gly Leu Ser Thr Ala Leu Gln Leu Phe Asp Asp Phe
115 120 125

Lys Lys Met Arg Glu Gln Ile Gly Gln Thr His Arg Val Cys Leu Leu
130 135 140

Ile Cys Asn Ser Pro Pro Tyr Leu Leu Pro Ala Val Glu Ser Thr Thr
145 150 155 160

Tyr Ser Gly Cys Thr Thr Glu Asn Leu Val Gln Gln Ile Gly Glu Arg
165 170 175

Gly Ile His Phe Ser Ile Val Ser Pro Arg Lys Leu Pro Ala Leu Arg
180 185 190

Leu Leu Phe Glu Lys Ala Ala Pro Pro Ala Leu Leu Glu Pro Leu Gln
195 200 205

Pro Pro Thr Asp Val Ser Gln Asp Pro Arg His Met Val Leu Val Arg
210 215 220

Gly Leu Val Leu Pro Val Gly Gly Gly Ser Ala Leu Gly Pro Leu Gln
225 230 235 240

Ser Lys Gln Pro Val Pro Leu Pro Pro Ala Ala Pro Ser Gly Ala Thr
245 250 255

Leu Ser Ala Ala Pro Gln Gln Pro Leu Pro Pro Val Pro Pro Gln Tyr
260 265 270

Gln Val Pro Gly Asn Leu Ser Ala Ala Gln Val Ala Ala Gln Asn Ala
275 280 285

Val Glu Ala Ala Lys Asn Gln Lys Ala Gly Leu Gly Pro Arg Phe Ser
290 295 300

Pro Ile Thr Pro Leu Gln Gln Ala Ala Pro Gly Val Gly Pro Pro Phe
305 310 315 320

Ser Gln Ala Pro Ala Pro Gln Leu Pro Pro Gly Pro Pro Gly Ala Pro
325 330 335

Lys Pro Pro Pro Ala Ser Gln Pro Ser Leu Val Ser Thr Val Ala Pro
340 345 350

Gly Ser Gly Leu Ala Pro Thr Ala Gln Pro Gly Ala Pro Ser Met Ala
355 360 365

Gly Thr Val Ala Pro Gly Gly Val Ser Gly Pro Ser Pro Ala Gln Leu
370 375 380

Gly Ala Pro Ala Leu Gly Gly Gln Gln Ser Val Ser Asn Lys Leu Leu
385 390 395 400

Ala Trp Ser Gly Val Leu Glu Trp Gln Glu Lys Pro Lys Pro Ala Ser
405 410 415

Val Asp Ala Asn Thr Lys Leu Thr Arg Ser Leu Pro Cys Gln Val Tyr
420 425 430

Val Asn His Gly Glu Asn Leu Lys Thr Glu Gln Trp Pro Gln Lys Leu
435 440 445

Ile Met Gln Leu Ile Pro Gln Gln Leu Leu Thr Thr Leu Gly Pro Leu
450 455 460

Phe Arg Asn Ser Arg Met Val Gln Phe His Phe Thr Asn Lys Asp Leu
465 470 475 480

Glu Ser Leu Lys Gly Leu Tyr Arg Ile Met Gly Asn Gly Phe Ala Gly
485 490 495

Cys Val His Phe Pro His Thr Ala Pro Cys Glu Val Arg Val Leu Met
500 505 510

Leu Leu Tyr Ser Ser Lys Lys Lys Ile Phe Met Gly Leu Ile Pro Tyr
515 520 525

Asp Gln Ser Gly Phe Val Asn Gly Ile Arg Gln Val Ile Thr Asn His
 530 535 540

Lys Gln Val Gln Gln Gln Lys Leu Glu Gln Gln Gln Arg Gly Met Gly
 545 550 555 560

Gly Gln Gln Ala Pro Pro Arg Ala Gly Ala His Ser Gly Gly Pro Ser
 565 570 575

Gln Ala Leu Thr Glu Ser Ala Pro Ala Pro Pro Thr Ala Ala Pro Ala
 580 585 590

Ser Gly Tyr Arg Arg Gly Leu Trp Gly His Gly Ala Ala Pro Ala Pro
 595 600 605

Arg Tyr Cys Pro Ala Pro Ala Arg Cys Pro Ser Arg Pro Ser Trp Ser
 610 615 620

Ser Phe Trp Pro Thr Pro Ser Trp Thr His Pro Ser Ala Pro Glu Pro
 625 630 635 640

Trp Gly Gln Pro Ser Ala Ala Lys Pro Pro Pro Gln Pro Thr Thr Ala
 645 650 655

Ala Asp Trp Gly Ala Pro Thr Pro Gly Leu Pro Pro Pro Pro Ala Gln
 660 665 670

Ser Trp Pro Ala Gln Leu Pro Pro Arg Ala Pro Leu Pro Gly Lys Gly
 675 680 685

Thr Arg Gly Arg Ala Glu Val Trp Thr Glu Cys Pro Ser Ser Ser Trp
 690 695 700

Ala Arg Ala Pro Arg Pro Ser Ala Pro Gly Lys
 705 710 715

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27 December 2002 (27.12.2002)

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- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

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(54) Title: **IN SILICO SCREENING FOR PHENOTYPE-ASSOCIATED EXPRESSED SEQUENCES**

(57) Abstract: The present invention provides methods for determining whether a nucleic acid sequence is a marker for a phenotype or cell type of interest which comprises providing a database of expressed sequence tag sequences (EST's) from the species; placing said EST's in groups termed clusters based on homology of EST's within each cluster; determining for each cluster the total number of EST's within said cluster; ordering said clusters sequentially based on the number of EST's in each cluster; dividing said ordered clusters into subranges based on the number of EST's per cluster; determining for each cluster subrange obtained from step (e) the number EST's within said cluster which are expressed in said predetermined cell type of interest; calculating according to a normal distribution the number of clusters in each subrange expected to contain a predetermined threshold percentage of EST's expressed in said cell type of interest, wherein said threshold percentage is a percentage from about 10% to about 100%; determining the number of clusters in each subrange observed to contain said predetermined threshold percentage of EST's expressed in said predetermined cell type; and identifying subranges having an observed number of clusters that meet said predetermined threshold percentage greater than the number of clusters expected to meet said predetermined threshold percentage for the subrange according to normal distribution; wherein if the percentage of EST's expressed in said cell type of interest in a cluster identified is equal to or greater than said predetermined threshold percentage, the cluster contains a nucleic acid that is a marker for the cell type of interest.

INTERNATIONAL SEARCH REPORT

Int'l Application No
PCT/IB 02/04189

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 G06F19/00 A61K39/395

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 G06F A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	VASMATZIS G: "Discovery of three genes specifically expressed in human prostate by expressed sequence tag database analysis" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE, WASHINGTON, US, vol. 95, January 1998 (1998-01), pages 300-304, XP002151634 ISSN: 0027-8424 cited in the application abstract page 300 - page 301 ----- -/--	1,40,47

☒ Further documents are listed in the continuation of box C.

☐ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

18 November 2003

Date of mailing of the international search report

11.02.2004

Name and mailing address of the ISA

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Authorized officer

Chabros, C

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB 02/04189

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-21, 40-55

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims: 1-21,40-55

relates to a method for determining nucleic acid markers for a predetermined phenotype or cell type of interest, consisting of algorithmic steps.
Independent claims 40 and 47 define embodiments of independent claim 1.

Inventions 2-202: claims 22-39 (all partially)

relate to nucleic acid sequences identified by SEQ ID NOs 9-141, cited in claim 24, and corresponding amino acid sequences, cited in claim 29.
